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OM protein - protein search, using sw model

Run on: July 23, 2004, 12:41:46 ; Search time 52 Seconds
(without alignments)
48.902 Million cell updates/sec

Title: US-09-458-298b-711

Perfect score: 44

Sequence: 1 KVAELVHFL 9

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq_29Jan04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	100.0	9	2 AAR73095	Aar73095 Antigen f
2	44	100.0	9	2 AAR73849	Aar73849 Antigen f
3	44	100.0	9	2 AAW70041	Aaw70041 MAGE 3 an
4	44	100.0	9	2 AAY47403	Aay47403 Immunogen
5	44	100.0	9	4 AAG84845	Asg84845 MAGE3 HLA
6	44	100.0	9	4 AAG84677	Asg84677 MAGE3 cro
7	44	100.0	9	4 AAG84835	Asg84835 MAGE3 A2
8	44	100.0	9	4 AAB99697	Aab99697 HLA A2 bi
9	44	100.0	9	4 AAB62400	Asg62400 Immunogen
10	44	100.0	9	4 AAB31314	Aab31314 Exemplary
11	44	100.0	9	4 AAB82008	Aab82008 HLA-A2 bi
12	44	100.0	9	5 AAE31199	Aae31199 Human mag
13	44	100.0	9	5 AAE31251	Aae31251 Human mag
14	44	100.0	9	6 ABU04441	Abu04441 Human exp
15	44	100.0	9	6 ABU04429	Abu04429 Human exp
16	44	100.0	9	6 ABU04444	Abu04444 Human exp
17	44	100.0	9	6 ABU04428	Abu04428 Human exp
18	44	100.0	9	6 ABU04451	Abu04451 Human exp
19	44	100.0	9	6 ABU04437	Abu04437 Human exp
20	44	100.0	9	6 ABU04439	Abu04439 Human exp
21	44	100.0	9	6 ABU04440	Abu04440 Human exp
22	44	100.0	9	6 ABU03321	Abu03321 Human exp
23	44	100.0	9	6 ABU04427	Abu04427 Human exp
24	44	100.0	9	6 ABU04435	Abu04435 Human exp
25	44	100.0	10	2 AAR73850	Aar73850 Antigen f

26	44	100.0	10	2 AAW70038	Aaw70038 MAGE 3 an
27	44	100.0	10	2 AAY47162	Aay47162 Immunogen
28	44	100.0	10	4 AAG84678	Asg84678 MAGE3 cro
29	44	100.0	10	4 AAG84836	Asg84836 MAGE3 A2
30	44	100.0	10	6 ABU04436	Abu04436 Human exp
31	44	100.0	10	6 ABU04442	Abu04442 Human exp
32	44	100.0	10	6 ABU04450	Abu04450 Human exp
33	44	100.0	10	6 ABU04438	Abu04438 Human exp
34	44	100.0	10	6 ABU04443	Abu04443 Human exp
35	44	100.0	15	3 AAB08828	Aab08828 Amino aci
36	44	100.0	15	4 AAG84626	Asg84626 MAGE3 DR
37	44	100.0	15	6 ABU04426	Abu04426 Human exp
38	44	100.0	15	6 ABU04434	Abu04434 Human exp
39	44	100.0	16	2 AAY01721	Aay01721 Peptide d
40	44	100.0	16	3 AAY92313	Aay92313 MAGE-A3 a
41	44	100.0	16	3 AAB02566	Aab02566 MAGE-A3 H
42	44	100.0	16	6 ABU04446	Abu04446 Human exp
43	44	100.0	16	6 ABU04424	Abu04424 Human exp
44	44	100.0	16	6 ABU04452	Abu04452 Human exp
45	44	100.0	30	5 AAU85051	Aau85051 Human MAG

ALIGNMENTS

RESULT 1

AAR73095
ID AAR73095 standard; peptide; 9 AA.

XX AAR73095;

DT 25-MAR-2003 (revised)

DT 16-JUN-1995 (first entry)

XX

DE Antigen fragment 1 from MAGE3 has binding affinity for HLA-2.1.

XX antigen; epitope; immunogenic target protein; PSA; HBVc; HBVs; EBV; HIV1;
XX plasma specific antigen; hepatitis B virus; Epstein Barr;
XX human immunodeficiency virus; human papilloma virus; p53; c-ERB2; MAGE-1;
XX melanoma antigen-1; core antigen; surface antigen;
XX pharmaceutical composition; in vivo; ex vivo; therapeutic; diagnostic;
XX MHC class I molecule; major histocompatibility complex; HLA-A2.1; 9mer;
XX 10mer; anchor; human leukocyte antigen; PLP; 8mer; algorithm prediction;
XX MBP; CMV; cytomegalovirus; HSV; herpes simplex virus; influenza A; M1.
XX Homo sapiens.

OS

XX WO9420127-A1.

XX PD 15-SEP-1994.

XX PF 04-MAR-1994; 94WO-US002353.

XX PR 05-MAR-1993; 93US-00027146.

XX PR 04-JUN-1993; 93US-00073205.

XX PR 29-NOV-1993; 93US-00159184.

XX (CYTE-) CYTEL CORP.

XX PI Grey HM, Sette A, Sidney J, Kast W;

XX WPI; 1994-302678/37.

XX DR Immunogenic peptide(s) having an HLA-A2.1 binding motif - used for

XX treatment or prophylaxis of cancer, virus infection or autoimmune

XX diseases.

XX PT Disclosure; Page 90; 138pp; English.

XX PS AAR73058-121 are potential peptide binders of HLA-A2.1 motif. Using

XX CC motifs disclosed in the invention, these peptides were screened for

XX further motifs. Only peptides with binding affinity of at least 1%

XX (binding affinity is expressed as an IC50 value) as compared to the

CC standard peptide (AAR71293) in assays. This peptide from the human
CC melanoma antigen has a binding value of 0.2200. The peptides of the
CC invention can induce cytotoxic T lymphocytes which can react with target
CC cells. They can be used for the treatment or prophylaxis of cancer, eg.
CC prostate cancer or lymphoma, etc. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
SQ Sequence 9 AA;
Query Match 100.0%; Score 44; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KVAELVHFL 9
DB 1 KVAELVHFL 9
RESULT 2
ID AAR73849 standard; peptide; 9 AA.
XX AAR73849;
AC AAR73849;
XX
DT 25-MAR-2003 (revised)
DT 22-JUN-1995 (first entry)
XX
DE Antigen fragment 165, from MAGE3 has binding affinity for HLA-2.1.
XX
KW antigen; epitope; immunogenic target protein; PSA; HBVc; HBVs; EBV; HIV1;
KW plasma specific antigen; hepatitis B virus; Epstein Barr;
KW human immunodeficiency virus; human papilloma virus; p53; c-ERB2; MAGE-1;
KW melanoma antigen-1; core antigen; surface antigen;
KW pharmaceutical composition; in vivo; ex vivo; therapeutic; diagnostic;
KW MHC class I molecule; major histocompatibility complex; HLA-A2.1; 9mer;
KW 10mer; anchor; human leukocyte antigen; PLP; 8mer; algorithm prediction;
KW MBP; CMV; cytomegalovirus; HSV; herpes simplex virus; Influenza A; M1;
KW LCMV.
XX
OS Homo sapiens.
XX
PN WO9420127-A1.
XX
PD 15-SEP-1994.
XX
PF 04-MAR-1994; 94WO-US002353.
XX
PR 05-MAR-1993; 93US-00027146.
PR 04-JUN-1993; 93US-00073205.
PR 29-NOV-1993; 93US-00159184.
XX
PA (CYTE-) CYTEL CORP.
XX
PI Grey HM, Sette A, Sidney J, Kast W;
XX
DR WPI; 1994-302678/37.
XX
PT Immunogenic peptide(s) having an HLA-A2.1 binding motif - used for
PT treatment or prophylaxis of cancer, virus infection or autoimmune
PT diseases.
XX
XX Disclosure; Page 86; 138pp; English.
XX
PS AAR73685-876 are potential peptide binders of HLA-A2.1 motif. Using
CC motifs disclosed in the invention, these peptides were screened for
CC further motifs. Only peptides with binding affinity of at least 1%
CC (binding affinity is expressed as an IC50 value) as compared to the
CC standard peptide (AAR71293) in assays. This peptide from MAGE3 has a
CC binding value of 0.0550. The peptides of the invention can induce
CC cytotoxic T lymphocytes which can react with target cells. They can be
CC used for the treatment or prophylaxis of cancer, eg. prostate cancer or
CC lymphoma, etc. (Updated on 25-MAR-2003 to correct PN field.)
XX

SQ Sequence 9 AA;
Query Match 100.0%; Score 44; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KVAELVHFL 9
DB 1 KVAELVHFL 9
RESULT 3
ID AAW70041 standard; peptide; 9 AA.
XX AAW70041;
AC AAW70041;
XX
DT 22-OCT-1998 (first entry)
XX
DE MAGE 3 antigen derived HLA-A2.1 binding peptide 7 (residues 112-120).
XX
KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
KW human leukocyte antigen; HLA; tumour associated antigen; cancer;
KW antigen presenting cell; APC; immunogenic peptide; immune disorder;
KW viral infection; AIDS; hepatitis; bacterial infection; malaria;
KW fungal infection; tuberculosis; melanoma; MAGE antigen.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9833889-A1.
XX
PD 06-AUG-1998.
XX
PF 30-JAN-1998; 98WO-US001959.
XX
PR 31-JAN-1997; 97US-0036696P.
XX
PA (EPIM-) EPIMMUNE INC.
XX
PI Teai V, Southwood S, Sidney J, Sette A, Celis E;
XX
DR WPI; 1998-437445/37.
XX
PT Production of antigen-specific cytotoxic T cells - by incubating
PT immunogenic peptide(s) from antigen that binds class I major
PT histocompatibility complex molecules with pre-treated antigen presenting
PT cells.
XX
PS Example 5; Page 72; 104pp; English.
XX
XX Sequences shown in AAW70027 to AAW70043 represent peptides derived from
CC MAGE2 and MAGE3 antigens. The peptides can bind to a human leukocyte
CC antigen (HLA), HLA-A2.1 and are used to exemplify the method of invention
CC of producing antigen-specific cytotoxic T cells (CTLs) in vitro. The
CC method comprises contacting immunogenic peptides from an antigen that
CC binds class I major histocompatibility complex (MHC) molecules with
CC antigen presenting cells (APCs) pretreated with pretreatment growth
CC factors, and incubating the APCs with purified CD8 cells in the presence
CC of at least 2 incubation growth factors, thereby producing antigen-
CC specific CTLs. A method for specifically killing target cells in a human
CC patient is also provided which comprises obtaining a fluid sample
CC containing CTLs from a patient, contacting the cytotoxic T cells with
CC APCs pretreated with pre-treatment growth factors, where the APCs
CC comprise class I MHC molecules. The pretreated APCs are incubated with
CC the cytotoxic growth factors, thereby producing activated CTLs which are
CC contacted with a carrier to form a composition. The composition can then
CC be administered to the patient. The activated CTLs can be used for
CC treating cancers, immune disorders, viral infections, AIDS, hepatitis,
CC bacterial infection, fungal infection, malaria or tuberculosis
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 44; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVAELVHFL 9
 DB 1 KVAELVHFL 9
 |||||

RESULT 4
 AAY47403
 ID AAY47403 standard; peptide; 9 AA.
 AC AAY47403;
 XX
 DT 01-DEC-1999 (first entry)
 XX
 DE Immunogenic peptide having a human leukocyte antigen binding motif #2014.
 XX
 KW Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
 KW immune response; T cell activation; major histocompatibility complex;
 KW cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;
 KW prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
 KW vaccine; immunisation.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO9945954-A1.
 XX
 PD 16-SEP-1999.
 XX
 XX 13-MAR-1998; 98WO-US005039.
 XX
 XX 13-MAR-1998; 98WO-US005039.
 XX
 XX (EPIM-) EPIMUNE INC.
 XX
 XX Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;
 PI
 XX WPI; 1999-551214/46.
 DR
 XX
 XX New immunogenic peptides with HLA binding motif, useful in treatment and
 PT diagnosis of cancers and viral diseases.
 XX
 PS Claim 1; Page 107; 150pp; English.
 XX
 XX AAY45390 to AAY48214 represent specifically claimed immunogenic peptides
 CC having a human major histocompatibility complex (MHC) Class I (also known
 CC as human leukocyte antigen (HLA)) binding motif. The immunogenic peptides
 CC can bind to a specific HLA allele (i.e. HLA-A subtypes HLA-A2.1, A1, A3.2
 CC or A24.1 or HLA-B or C) and induce a cytotoxic T cell response against
 CC the antigen from which the peptide is derived. Cytotoxic T lymphocytes
 CC (CTLs) which destroy antigen-bearing cells are normally induced by an
 CC antigen in the form of a peptide fragment bound to a HLA molecule, rather
 CC than the intact foreign antigen itself, and are particularly important in
 CC tumour rejection and in fighting viral infections. The peptides are
 CC therefore useful therapeutically to treat or prevent viral infections and
 CC cancers in mammals (especially humans) e.g. prostate cancer, hepatitis B
 CC and C, AIDS, and renal carcinoma. They can be administered as vaccines to
 CC elicit an immune response in individuals susceptible or otherwise at risk
 CC of viral infection or cancer, or used to treat chronic or acute
 CC conditions. They are also useful diagnostically, and can be used to
 CC induce a cytotoxic T cell response, by contacting a cytotoxic T cell with
 CC the peptide e.g. to produce CTLs ex vivo for infusion back into a
 CC patient. The polynucleotides encoding the immunogenic peptides are also
 CC useful therapeutically and for immunisation as above
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 44; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVAELVHFL 9
 DB 1 KVAELVHFL 9
 |||||

QY 1 KVAELVHFL 9
 DB 1 KVAELVHFL 9
 |||||

RESULT 5
 AAG84845
 ID AAG84845 standard; peptide; 9 AA.
 XX
 AC AAG84845;
 XX
 DT 10-SEP-2001 (first entry)
 XX
 DE MAGE3 HLA-A2 supermotif-bearing peptide #1.
 XX
 KW Human; human leukocyte antigen; HLA epitope; cytotoxic T lymphocyte; CTL;
 KW MAGE2; MAGE3; melanoma antigen gene; immune response; vaccine; cancer;
 KW cytostatic; immunostimulant.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200142267-A1.
 XX
 XX 14-JUN-2001.
 PD
 XX 11-DEC-2000; 2000WO-US033545.
 PF
 XX 10-DEC-1999; 99US-00458298.
 PR
 XX (EPIM-) EPIMUNE INC.
 PA
 XX Fikes J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E;
 PI Keogh E;
 PI
 XX WPI; 2001-375002/39.
 DR
 XX An isolated prepared MAGE2/3 epitope (I) for use in pharmaceuticals for
 PT the treatment and prevention of cancer.
 PT
 PS Claim 1; Page 161; 171pp; English.
 XX
 XX The present invention describes MAGE2/3 epitopes (I). Also described are:
 CC (1) a clonal cytotoxic T lymphocyte (CTL) that is cultured in vivo and
 CC binds to a complex of (I); (2) a peptide (II) comprising (I) and a second
 CC epitope and has less than 50 contiguous amino acids; (3) a vaccine
 CC composition comprising (II), a unit dose of a peptide with at least 50
 CC contiguous amino acids with 100% identity to the native peptide sequence
 CC of MAGE2/3, and a pharmaceutical excipient; (4) an isolated nucleic acid
 CC encoding (I); and (5) an isolated nucleic acid encoding (II). (I) has
 CC cytostatic activity, and can be used in vaccines and as an
 CC immunostimulant. A vaccine of (3) is useful for the treatment and
 CC prevention of cancer. (I) is useful for monitoring or evaluating an
 CC immune response by incubating a T-lymphocyte sample from a patient with
 CC (I) that binds to an human leukocyte antigen (HLA) allele present in the
 CC patient and detecting the presence of the T-lymphocyte that binds to the
 CC peptide. The vaccine allows the opportunity to combine epitopes derived
 CC from multiple tumour-associated molecules reducing the likelihood of
 CC tumour escape due to antigen loss. AAG84515 to AAG84909 and AAG99725
 CC represent amino acid sequences used in the exemplification of the present
 CC invention
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 44; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVAELVHFL 9
 DB 1 KVAELVHFL 9
 |||||

```

RESULT 6
AAG84677
ID AAG84677 standard; peptide; 9 AA.
XX
AC AAG84677;
XX
XX 10-SEP-2001 (first entry)
XX
DE MAGE3 crossbinding data A2 supermotif peptide #1.
XX
XX Human; human leukocyte antigen; HLA epitope; cytotoxic T lymphocyte; CTL;
KW MAGE2; MAGE3; melanoma antigen gene; immune response; vaccine; cancer;
KW cytostatic; immunostimulant.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200142267-A1.
XX
PD 14-JUN-2001.
XX
PF 11-DEC-2000; 2000WO-US033545.
XX
PR 10-DEC-1999; 99US-00458298.
XX
PA (EPIM-) EPIMMUNE INC.
XX
PI Fikes J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E;
PI Keogh E;
XX
DR WPI; 2001-375002/39.
XX
PT An isolated prepared MAGE2/3 epitope (I) for use in pharmaceuticals for
PT the treatment and prevention of cancer.
XX
PS Example 2; Page 151; 171pp; English.
XX
CC The present invention describes MAGE2/3 epitopes (I). Also described are:
CC (1) a clonal cytotoxic T lymphocyte (CTL) that is cultured in vivo and
CC binds to a complex of (I); (2) a peptide (II) comprising (I) and a second
CC epitope and has less than 50 contiguous amino acids; (3) a vaccine
CC composition comprising (II), a unit dose of a peptide with at least 50
CC contiguous amino acids with 100% identity to the native peptide sequence
CC of MAGE2/3, and a pharmaceutical excipient; (4) an isolated nucleic acid
CC encoding (I); and (5) an isolated nucleic acid encoding (II). (I) has
CC cytostatic activity, and can be used in vaccines and as an
CC immunostimulant. A vaccine of (3) is useful for the treatment and
CC prevention of cancer. (I) is useful for monitoring or evaluating an
CC immune response by incubating a T-lymphocyte sample from a patient with
CC (I) that binds to an human leukocyte antigen (HLA) allele present in the
CC patient and detecting the presence of the T-lymphocyte that binds to the
CC peptide. The vaccine allows the opportunity to combine epitopes derived
CC from multiple tumour-associated molecules reducing the likelihood of
CC tumour escape due to antigen loss. AAG84515 to AAG84909 and AAB99725
CC represent amino acid sequences used in the exemplification of the present
CC invention
XX
SQ Sequence 9 AA;
Query Match 100.0%; Score 44; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KVAELVHFL 9
DB 1 KVAELVHFL 9
RESULT 7
AAG84835
ID AAG84835 standard; peptide; 9 AA.
XX
AC AAG84835;
XX
XX 10-SEP-2001 (first entry)
XX
DE MAGE3 A2 supermotif peptide #1.
XX
XX Human; human leukocyte antigen; HLA epitope; cytotoxic T lymphocyte; CTL;
KW MAGE2; MAGE3; melanoma antigen gene; immune response; vaccine; cancer;
KW cytostatic; immunostimulant.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200142267-A1.
XX
PD 14-JUN-2001.
XX
PF 11-DEC-2000; 2000WO-US033545.
XX
PR 10-DEC-1999; 99US-00458298.
XX
PA (EPIM-) EPIMMUNE INC.
XX
PI Fikes J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E;
PI Keogh E;
XX
DR WPI; 2001-375002/39.
XX
PT An isolated prepared MAGE2/3 epitope (I) for use in pharmaceuticals for
PT the treatment and prevention of cancer.
XX
PS Claim 1; Page 160; 171pp; English.
XX
CC The present invention describes MAGE2/3 epitopes (I). Also described are:
CC (1) a clonal cytotoxic T lymphocyte (CTL) that is cultured in vivo and
CC binds to a complex of (I); (2) a peptide (II) comprising (I) and a second
CC epitope and has less than 50 contiguous amino acids; (3) a vaccine
CC composition comprising (II), a unit dose of a peptide with at least 50
CC contiguous amino acids with 100% identity to the native peptide sequence
CC of MAGE2/3, and a pharmaceutical excipient; (4) an isolated nucleic acid
CC encoding (I); and (5) an isolated nucleic acid encoding (II). (I) has
CC cytostatic activity, and can be used in vaccines and as an
CC immunostimulant. A vaccine of (3) is useful for the treatment and
CC prevention of cancer. (I) is useful for monitoring or evaluating an
CC immune response by incubating a T-lymphocyte sample from a patient with
CC (I) that binds to an human leukocyte antigen (HLA) allele present in the
CC patient and detecting the presence of the T-lymphocyte that binds to the
CC peptide. The vaccine allows the opportunity to combine epitopes derived
CC from multiple tumour-associated molecules reducing the likelihood of
CC tumour escape due to antigen loss. AAG84515 to AAG84909 and AAB99725
CC represent amino acid sequences used in the exemplification of the present
CC invention
XX
SQ Sequence 9 AA;
Query Match 100.0%; Score 44; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KVAELVHFL 9
DB 1 KVAELVHFL 9
RESULT 8
AAB99697
ID AAB99697 standard; peptide; 9 AA.
XX
XX AAB99697;
AC
XX
XX 06-SEP-2001 (first entry)
DT
DE HLA A2 binding CTL epitope peptide from MAGE3 SEQ ID NO:18.

```


KW Human leukocyte antigen A2 binding peptide; HLA class I A2; CTL;
 KW cytotoxic T-cell lymphocyte; tumour associated antigen; CEA; HER2/neu;
 KW MAGE2; MAGE3; p53; vaccine; cancer; cytostatic; immunomodulator;
 KW immunotherapy; immune response.
 OS Homo sapiens.
 XX
 XX WO200141741-A1.
 XX
 XX 14-JUN-2001.
 XX
 XX 13-DEC-2000; 2000WO-US034318.
 XX
 XX 13-DEC-1999; 99US-0170448P.
 XX 05-APR-2000; 2000US-00543608.
 XX 30-MAY-2000; 2000US-00583200.
 XX
 XX (EPIM-) EPIMMUNE INC.
 XX
 XX Fikes J, Sette A, Sidney J, Southwood S, Celis E, Keogh E;
 PI Chesnut R;
 XX
 XX WPI; 2001-381489/40.
 XX
 XX Compositions for use in a vaccine for treating, e.g., breast, lung and
 PT colon cancer comprises at least one peptide that comprises an isolated
 PT epitope of a tumor-associated antigen.
 XX
 XX Claim 1; Page 76; 86pp; English.
 XX
 CC The present invention describes a composition (I) comprising at least one
 CC peptide that comprises an isolated, prepared epitope consisting of a
 CC sequence selected from 25 short amino acid sequences given in AAB99680 to
 CC AAB99704. Also described are: (1) a composition (II) comprising one or
 CC more peptides, and further comprising at least two epitopes selected from
 CC the 25 short amino acid sequences (as above), where each of the one or
 CC more peptides comprise less than 50 contiguous amino acids that have 100%
 CC identity with a native peptide sequence; and (2) a vaccine composition
 CC (III) comprising an epitope selected from the 25 short amino acid
 CC sequences (as above) and a pharmaceutical excipient. (I) has cytostatic
 CC and immunomodulatory activities and can be used in vaccine production and
 CC immunotherapy. The peptide epitope compositions (I)-(III) are useful for
 CC monitoring an immune response to a tumour associated antigen or when one
 CC or more peptides are combined to create a vaccine (III) that stimulates
 CC the cellular arm of the immune system. In particular, the vaccine
 CC mediates immune responses against tumours in individuals who bear an
 CC allele of the human leukocyte antigen (HLA)-A2 supertype and improve the
 CC standard of care for patients being treated for breast, colon, or lung
 CC cancer
 XX
 XX Sequence 9 AA;
 SQ
 Query Match 100.0%; Score 44; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KVAELVHFL 9
 Db 1 KVAELVHFL 9
 |||||
 RESULT 9
 AAG62400
 ID AAG62400 standard; peptide; 9 AA.
 XX
 XX AAG62400;
 AC
 XX
 XX 03-SEP-2001 (first entry)
 DT
 XX
 XX Immunogenic peptide MAGE3.112 SEQ ID 4.
 DE
 XX Class I epitope; immunogenic; heteroclitic analogue; immune response;
 KW

KW antigen display; viral disease; cancer.
 XX
 OS Synthetic.
 XX
 XX WO200136452-A2.
 XX
 XX 25-MAY-2001.
 XX
 XX 20-NOV-2000; 2000WO-US031856.
 XX
 XX 18-NOV-1999; 99US-0166529P.
 XX 06-OCT-2000; 2000US-0239008P.
 XX
 XX (EPIM-) EPIMMUNE INC.
 XX
 XX Tangri S, Sette A, Ishioka G;
 PI WPI; 2001-355609/37.
 XX
 XX Enhancing immunogenicity of peptide containing class I epitope, useful
 PT for treating cancer, comprises providing (semi-)conservative amino acid
 PT substitutions at specified positions of these epitopes.
 XX
 XX Disclosure; Fig 1A; 96pp; English.
 XX
 CC This invention relates to a method of enhancing the immunogenicity of a
 CC peptide, where the peptide contains a class I epitope. The invention
 CC includes methods for preparing peptides containing epitopes which have
 CC enhanced ability to effect an immune response (compared to wild-type
 CC epitopes). The peptides are referred to as heteroclitic analogues. The
 CC method is useful for eliciting an immune response by contacting CTLs with
 CC the immunogenically enhanced peptide in vitro in the presence of an
 CC antigen presenting cell, or by administering to a subject a nucleic acid
 CC molecule comprising a nucleotide sequence encoding the peptide. The
 CC peptides are useful as reagents to evaluate an immune response and the
 CC efficacy of the vaccine, and for making antibodies. The heteroclitic
 CC analogues are useful in immunological compositions for the treatment of
 CC viral diseases, cancer, and other conditions which are characterised by
 CC displayed antigens on target cells. The present sequence represents a
 CC class I epitope which may be used in the method of the invention
 XX
 XX Sequence 9 AA;
 SQ
 Query Match 100.0%; Score 44; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KVAELVHFL 9
 Db 1 KVAELVHFL 9
 |||||
 RESULT 10
 AAB31314
 ID AAB31314 standard; peptide; 9 AA.
 XX
 XX AAB31314;
 AC
 XX
 XX 20-APR-2001 (first entry)
 DT
 XX
 XX Exemplary antigen characteristic of tumours and derived from MAGE-A3.
 DE
 XX MAGE-A1; HLA; human leukocyte antigen; CD4+ T lymphocyte; cancer;
 KW MAGE-A1 HLA class II-binding protein; vaccine.
 KW
 XX Homo sapiens.
 OS
 XX WO200078806-A1.
 XX
 XX 28-DEC-2000.
 XX
 XX 14-JUN-2000; 2000WO-US016287.
 XX
 XX

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PR 18-JUN-1999; 99US-00336091.
XX (LUDW-) LUDWIG INST CANCER RES.
XX Van Snick J, Lethe B, Chaux P, Boon-Palleur T, Van Der Bruggen P;
XX WPI; 2001-102698/11.
XX
XX Novel MAGE-A1 human leukocyte antigen class II peptides which bind to and
PT are presented to the class II molecules, useful for inducing immune
PT response and treating cancers characterized by expression of MAGE-A1.
XX
XX Disclosure; Page 32; 78pp; English.
XX
XX AAB31302-59 represent exemplary antigens which are characteristic of
CC tumours. They can be used to enhance the immune response of vaccines
CC comprising peptides derived from human MAGE-A1 HLA (human leukocyte
CC antigen) class II-binding protein. Peptides derived from the MAGE-A1 HLA
CC binding protein stimulate the activity and proliferation of CD4+ T
CC lymphocytes. The MAGE-A1 HLA binding protein is useful as a diagnostic
CC agent for diagnosing a disorder characterized by expression of MAGE-A1.
CC The protein is used for treating a disorder characterized by expression
CC of MAGE-A1 such as cancers e.g. melanoma, squamous cell carcinomas,
CC colorectal carcinomas, osteosarcomas, and lymphocytic leukemias. Peptides
CC derived from the MAGE-A1 HLA binding protein are useful in the production
CC of anti-tumour vaccines
XX
XX Sequence 9 AA;
XX
XX Query Match 100.0%; Score 44; DB 4; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 1.4e+06;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 KVAELVHFL 9
XX Db 1 KVAELVHFL 9
XX
XX RESULT 11
XX AAB82008
XX ID AAB82008 standard; peptide; 9 AA.
XX AC AAB82008;
XX
XX 12-JUN-2001 (first entry)
XX
XX HLA-A2 binding peptide derived from MAGE-A3.
XX
XX Multiple myeloma; tumour rejection antigen precursor; MAGE; BAGE; GAGE;
XX LAGE; NY-ESO-1; PRAME; DAGE; human; HLA.
XX
XX Homo sapiens.
XX
XX US6210886-B1.
XX
XX 03-APR-2001.
XX
XX 30-OCT-1998; 98US-00183931.
XX
XX 04-FEB-1998; 98US-00018422.
XX
XX (LUDW-) LUDWIG INST CANCER RES.
XX
XX Van Baren N, Brasseur F, Boon-Palleur T;
XX WPI; 2001-289628/30.
XX
XX Detecting multiple myeloma in a patient, comprises contacting a nucleic
XX acid containing sample taken from bone marrow or blood with a
XX hybridization probe specific for a tumor rejection antigen precursor.
XX
XX Example 3; Col 11; 16pp; English.
XX

CC The present invention relates to a method for detecting multiple myeloma.
CC The method comprises contacting a nucleic acid containing a sample taken
CC from a bone marrow or blood of a patient, with a hybridisation probe
CC specific for a tumour rejection antigen precursor. Tumour rejection
CC antigen precursors used in the present invention are the MAGE family,
CC BAGE, GAGE, LAGE, NY-ESO-1 and PRAME (previously referred to as DAGE).
CC Expression of the tumour rejection antigen precursor indicates possible
CC multiple myeloma in the patient. The method can also be used for
CC monitoring the disease progress and course of therapeutic regime. The
CC present sequence is a peptide derived from a tumour rejection antigen
CC precursor, which was used in the method of the present invention
XX
XX Sequence 9 AA;
XX
XX Query Match 100.0%; Score 44; DB 4; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 1.4e+06;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 KVAELVHFL 9
XX Db 1 KVAELVHFL 9
XX
XX RESULT 12
XX AAE31199
XX ID AAE31199 standard; peptide; 9 AA.
XX AC AAE31199;
XX
XX 24-FEB-2003 (first entry)
XX
XX Human mage3 peptide #4.
XX
XX Human; T-lymphocyte; vaccine; viral infection; gene therapy; cancer.
XX
XX Homo sapiens.
XX
XX WO200272627-A2.
XX
XX 19-SEP-2002.
XX
XX 11-MAR-2002; 2002WO-EP002666.
XX
XX 09-MAR-2001; 2001US-0274250P.
XX
XX 14-MAY-2001; 2001US-0290353P.
XX
XX 18-MAY-2001; 2001US-0291610P.
XX
XX (CALL-) CALLISTOGEN AG.
XX
XX Wrede P, Walden P, Eichler-Mertens M, Filter M;
XX WPI; 2002-759836/82.
XX
XX Providing, identifying or optimizing peptides for inducing cytotoxic T-
XX lymphocytes and for treating cancer, comprises selecting conserved
XX regions in antigenic proteins and identifying CD8+ T-cell epitopes in the
XX protein.
XX
XX Disclosure; Page 9; 32pp; English.
XX
XX The invention relates to a method for providing, identifying or/and
XX optimising peptides which induce cytotoxic T-lymphocytes and to the uses
XX of the obtained peptides for vaccination. The method is useful for
XX providing, identifying and/or optimising peptides that are useful in
XX manufacturing a pharmaceutical composition for the induction of cytotoxic
XX T-lymphocytes, and for the prevention, treatment or diagnosis of cancer
XX or viral infections. The invention is also used in gene therapy. The
XX present sequence is human mage3 peptide used to illustrate the method of
XX the invention
XX
XX Sequence 9 AA;
XX
XX Query Match 100.0%; Score 44; DB 5; Length 9;
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Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVAELVHFL 9
Db 1 KVAELVHFL 9

RESULT 13
AAE31251
ID AAE31251 standard; peptide; 9 AA.
AC AAE31251;
DT 24-FEB-2003 (first entry)
DE Human mage9 peptide #4.
KW Human; T-lymphocyte; vaccine; viral infection; gene therapy; cancer.
OS Homo sapiens.
XX WO200272627-A2.
XX 19-SEP-2002.
XX 11-MAR-2002; 2002WO-EP002666.
XX 09-MAR-2001; 2001US-0274250P.
XX 14-MAY-2001; 2001US-0290353P.
XX 18-MAY-2001; 2001US-0291610P.
XX (CALL-) CALLISTOGEN AG.
XX Wrede P, Walden P, Eichler-Mertens M, Filter M;
XX WPI; 2002-759836/82.
XX Providing, identifying or optimizing peptides for inducing cytotoxic T-
XX lymphocytes and for treating cancer, comprises selecting conserved
XX regions in antigenic proteins and identifying CD8+ T-cell epitopes in the
XX protein.
XX Disclosure; Page 10; 32pp; English.
XX The invention relates to a method for providing, identifying or/and
XX optimising peptides which induce cytotoxic T-lymphocytes and to the uses
XX of the obtained peptides for vaccination. The method is useful for
XX providing, identifying and/or optimising peptides that are useful in
XX manufacturing a pharmaceutical composition for the induction of cytotoxic
XX T-lymphocytes, and for the prevention, treatment or diagnosis of cancer
XX or viral infections. The invention is also used in gene therapy. The
XX present sequence is human mage9 peptide used to illustrate the method of
XX the invention
XX Sequence 9 AA;
Query Match 100.0%; Score 44; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVAELVHFL 9
Db 1 KVAELVHFL 9

RESULT 14
ABU04441
ID ABU04441 standard; protein; 9 AA.
XX AC ABU04441;
XX 29-JAN-2003 (first entry)
DT 29-JAN-2003 (first entry)

XX Human expressed protein tag (EPT) #1107.
XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
XX protease; protease inhibitor; transporter; cytoskeletal protein;
XX receptor; transcription factor; cancer; MHC;
XX major histocompatibility complex; myeloma; colon cancer; gastric cancer;
XX adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX Homo sapiens.
XX WO200278524-A2.
XX 10-OCT-2002.
XX 28-MAR-2002; 2002WO-US009671.
XX 28-MAR-2001; 2001US-0279495P.
XX 21-MAY-2001; 2001US-0292544P.
XX 08-AUG-2001; 2001US-0310801P.
XX 01-OCT-2001; 2001US-0326370P.
XX 04-DEC-2001; 2001US-0336780P.
XX 20-FEB-2002; 2002US-0358985P.
XX (ZYCO-) ZYCOS INC.
XX Chicx RM, Tomlinson AJ, Urban RG;
XX WPI; 2003-040607/03.
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX cytoskeletal proteins, receptors or transcription factors), useful for
XX treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
XX leukemia.
XX Example 2; SEQ ID NO 1107; 134pp; English.
XX The invention describes a purified polypeptide, which comprises a
XX fragment of a kinase, phosphatase, protease, protease inhibitor,
XX transporter, cytoskeletal protein, receptor or transcription factor. The
XX polypeptide is useful as an immunogenic composition for eliciting in a
XX mammal an immunogenic response directed against any of the purified
XX polypeptide. The purified polypeptide, or the antibody that binds to this
XX polypeptide, is useful for treating cancer. The polypeptide is also
XX useful for identifying compounds that binds to a naturally processed
XX class I or class II MHC-binding polypeptide. The polypeptides and
XX polynucleotides are particularly useful for treating or preventing
XX myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
XX lymphoma or leukaemia. These are also useful for screening agents for
XX treating the above mentioned diseases. This sequence represents an
XX expressed protein tag (EPT) isolated from human tissue for translational
XX profiling. Note: This sequence does not appear in the printed
XX specification but was obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX Sequence 9 AA;
Query Match 100.0%; Score 44; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVAELVHFL 9
Db 1 KVAELVHFL 9

RESULT 15
ABU04429
ID ABU04429 standard; protein; 9 AA.
XX AC ABU04429;
XX 29-JAN-2003 (first entry)
DT 29-JAN-2003 (first entry)
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XX DE Human expressed protein tag (EPT) #1094.
XX DE
XX DE
KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX OS
XX OS Homo sapiens.
XX PN WO200278524-A2.
XX PD 10-OCT-2002.
XX PF
XX PF 28-MAR-2002; 2002WO-US009671.
XX PR 28-MAR-2001; 2001US-0279495P.
XX PR 21-MAY-2001; 2001US-0292544P.
XX PR 08-AUG-2001; 2001US-0310801P.
XX PR 01-OCT-2001; 2001US-0326370P.
XX PR 04-DEC-2001; 2001US-0336780P.
XX PR 20-FEB-2002; 2002US-0358985P.
XX PA (ZYCO-) ZYCOS INC.
XX PI Chicx RM, Tomlinson AJ, Urban RG;
XX PI WPI; 2003-040607/03.
XX DR
XX DR
XX PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX PT cytoskeletal proteins, receptors or transcription factors), useful for
XX PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
XX PT leukemia.
XX PS Example 2; SEQ ID NO 1094; 134pp; English.
XX CC The invention describes a purified polypeptide, which comprises a
XX CC fragment of a kinase, phosphatase, protease, protease inhibitor,
XX CC transporter, cytoskeletal protein, receptor or transcription factor. The
XX CC polypeptide is useful as an immunogenic composition for eliciting in a
XX CC mammal an immunogenic response directed against any of the purified
XX CC polypeptide. The purified polypeptide, or the antibody that binds to this
XX CC polypeptide, is useful for treating cancer. The polypeptide is also
XX CC useful for identifying compounds that binds to a naturally processed
XX CC class I or class II MHC-binding polypeptide. The polypeptides and
XX CC polynucleotides are particularly useful for treating or preventing
XX CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
XX CC lymphoma or leukaemia. These are also useful for screening agents for
XX CC treating the above mentioned diseases. This sequence represents an
XX CC expressed protein tag (EPT) isolated from human tissue for translational
XX CC profiling. Note: This sequence does not appear in the printed
XX CC specification but was obtained in electronic format directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 9 AA;

Query Match 100.0%; Score 44; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVAELVHFL 9
Db 1 KVAELVHFL 9

RESULT 18
ABU04451
ID ABU04451 standard; protein; 9 AA.
XX AC ABU04451;
XX DT 29-JAN-2003 (first entry)

Human expressed protein tag (EPT) #1117.
XX DE
XX DE
KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX OS
XX OS Homo sapiens.
XX PN WO200278524-A2.
XX PD 10-OCT-2002.
XX PF
XX PF 28-MAR-2002; 2002WO-US009671.
XX PR 28-MAR-2001; 2001US-0279495P.
XX PR 21-MAY-2001; 2001US-0292544P.
XX PR 08-AUG-2001; 2001US-0310801P.
XX PR 01-OCT-2001; 2001US-0326370P.
XX PR 04-DEC-2001; 2001US-0336780P.
XX PR 20-FEB-2002; 2002US-0358985P.
XX PA (ZYCO-) ZYCOS INC.
XX PI Chicx RM, Tomlinson AJ, Urban RG;
XX PI WPI; 2003-040607/03.
XX DR
XX DR
XX PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX PT cytoskeletal proteins, receptors or transcription factors), useful for
XX PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
XX PT leukemia.
XX PS Example 2; SEQ ID NO 1117; 134pp; English.
XX CC The invention describes a purified polypeptide, which comprises a
XX CC fragment of a kinase, phosphatase, protease, protease inhibitor,
XX CC transporter, cytoskeletal protein, receptor or transcription factor. The
XX CC polypeptide is useful as an immunogenic composition for eliciting in a
XX CC mammal an immunogenic response directed against any of the purified
XX CC polypeptide. The purified polypeptide, or the antibody that binds to this
XX CC polypeptide, is useful for treating cancer. The polypeptide is also
XX CC useful for identifying compounds that binds to a naturally processed
XX CC class I or class II MHC-binding polypeptide. The polypeptides and
XX CC polynucleotides are particularly useful for treating or preventing
XX CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
XX CC lymphoma or leukaemia. These are also useful for screening agents for
XX CC treating the above mentioned diseases. This sequence represents an
XX CC expressed protein tag (EPT) isolated from human tissue for translational
XX CC profiling. Note: This sequence does not appear in the printed
XX CC specification but was obtained in electronic format directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 9 AA;

Query Match 100.0%; Score 44; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVAELVHFL 9
Db 1 KVAELVHFL 9

RESULT 19
ABU04437
ID ABU04437 standard; protein; 9 AA.
XX AC ABU04437;
XX DT 29-JAN-2003 (first entry)

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```
XX DE Human expressed protein tag (EPT) #1103.
XX DE
XX KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
XX KW protease; protease inhibitor; transporter; cytoskeletal protein;
XX KW receptor; transcription factor; cancer; MHC;
XX KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
XX KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX OS Homo sapiens.
XX PN WO200278524-A2.
XX PD 10-OCT-2002.
XX PF 28-MAR-2002; 2002WO-US009671.
XX PR 28-MAR-2001; 2001US-0279495P.
XX PR 21-MAY-2001; 2001US-0292544P.
XX PR 08-AUG-2001; 2001US-0310801P.
XX PR 01-OCT-2001; 2001US-0326370P.
XX PR 04-DEC-2001; 2001US-0336780P.
XX PR 20-FEB-2002; 2002US-0358985P.
XX PA (ZYCO-) ZYCOS INC.
XX PI Chicx RM, Tomlinson AJ, Urban RG;
XX PD WPI; 2003-040607/03.
XX DR
XX PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX PT cytoskeletal proteins, receptors or transcription factors), useful for
XX PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
XX PT leukemia.
XX PS Example 2; SEQ ID NO 1103; 134pp; English.
XX CC The invention describes a purified polypeptide, which comprises a
XX CC fragment of a kinase, phosphatase, protease, protease inhibitor,
XX CC transporter, cytoskeletal protein, receptor or transcription factor. The
XX CC polypeptide is useful as an immunogenic composition for eliciting in a
XX CC mammal an immunogenic response directed against any of the purified
XX CC polypeptide. The purified polypeptide, or the antibody that binds to this
XX CC polypeptide, is useful for treating cancer. The polypeptide is also
XX CC useful for identifying compounds that binds to a naturally processed
XX CC class I or class II MHC-binding polypeptide. The polypeptides and
XX CC polynucleotides are particularly useful for treating or preventing
XX CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
XX CC lymphoma or leukaemia. These are also useful for screening agents for
XX CC treating the above mentioned diseases. This sequence represents an
XX CC expressed protein tag (EPT) isolated from human tissue for translational
XX CC profiling. Note: This sequence does not appear in the printed
XX CC specification but was obtained in electronic format directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 9 AA;
XX Query Match 100.0%; Score 44; DB 6; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 1.4e+06;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 KVAELVHFL 9
XX DB 1 KVAELVHFL 9
XX RESULT 20
XX ABU04439
XX ID ABU04439 standard; protein; 9 AA.
XX XX
XX AC ABU04439;
XX XX
XX DT 29-JAN-2003 (first entry)

XX DE Human expressed protein tag (EPT) #1105.
XX DE
XX KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
XX KW protease; protease inhibitor; transporter; cytoskeletal protein;
XX KW receptor; transcription factor; cancer; MHC;
XX KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
XX KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX OS Homo sapiens.
XX PN WO200278524-A2.
XX PD 10-OCT-2002.
XX PF 28-MAR-2002; 2002WO-US009671.
XX PR 28-MAR-2001; 2001US-0279495P.
XX PR 21-MAY-2001; 2001US-0292544P.
XX PR 08-AUG-2001; 2001US-0310801P.
XX PR 01-OCT-2001; 2001US-0326370P.
XX PR 04-DEC-2001; 2001US-0336780P.
XX PR 20-FEB-2002; 2002US-0358985P.
XX PA (ZYCO-) ZYCOS INC.
XX PI Chicx RM, Tomlinson AJ, Urban RG;
XX PD WPI; 2003-040607/03.
XX DR
XX PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX PT cytoskeletal proteins, receptors or transcription factors), useful for
XX PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
XX PT leukemia.
XX PS Example 2; SEQ ID NO 1105; 134pp; English.
XX CC The invention describes a purified polypeptide, which comprises a
XX CC fragment of a kinase, phosphatase, protease, protease inhibitor,
XX CC transporter, cytoskeletal protein, receptor or transcription factor. The
XX CC polypeptide is useful as an immunogenic composition for eliciting in a
XX CC mammal an immunogenic response directed against any of the purified
XX CC polypeptide. The purified polypeptide, or the antibody that binds to this
XX CC polypeptide, is useful for treating cancer. The polypeptide is also
XX CC useful for identifying compounds that binds to a naturally processed
XX CC class I or class II MHC-binding polypeptide. The polypeptides and
XX CC polynucleotides are particularly useful for treating or preventing
XX CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
XX CC lymphoma or leukaemia. These are also useful for screening agents for
XX CC treating the above mentioned diseases. This sequence represents an
XX CC expressed protein tag (EPT) isolated from human tissue for translational
XX CC profiling. Note: This sequence does not appear in the printed
XX CC specification but was obtained in electronic format directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 9 AA;
XX Query Match 100.0%; Score 44; DB 6; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 1.4e+06;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 KVAELVHFL 9
XX DB 1 KVAELVHFL 9
XX RESULT 21
XX ABU04440
XX ID ABU04440 standard; protein; 9 AA.
XX XX
XX AC ABU04440;
XX XX
XX DT 29-JAN-2003 (first entry)
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XX DE Human expressed protein tag (EPT) #1106.
XX KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
XX KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX OS Homo sapiens.
XX PN WO200278524-A2.
XX PD 10-OCT-2002.
XX PF 28-MAR-2002; 2002WO-US009671.
XX PR 28-MAR-2001; 2001US-0279495P.
XX PR 21-MAY-2001; 2001US-0292544P.
XX PR 08-AUG-2001; 2001US-0310801P.
XX PR 01-OCT-2001; 2001US-0326370P.
XX PR 04-DEC-2001; 2001US-0336780P.
XX PR 20-FEB-2002; 2002US-0358985P.
XX PA (ZYCO-) ZYCOS INC.
XX PI Chicx RM, Tomlinson AJ, Urban RG;
XX DR WPI; 2003-040607/03.
XX PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX PT cytoskeletal proteins, receptors or transcription factors), useful for
XX PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
XX PT leukemia.
XX PS Example 2; SEQ ID NO 1106; 134pp; English.
XX CC The invention describes a purified polypeptide, which comprises a
XX CC fragment of a kinase, phosphatase, protease, protease inhibitor,
XX CC transporter, cytoskeletal protein, receptor or transcription factor. The
XX CC polypeptide is useful as an immunogenic composition for eliciting in a
XX CC mammal an immunogenic response directed against any of the purified
XX CC polypeptide. The purified polypeptide, or the antibody that binds to this
XX CC polypeptide, is useful for treating cancer. The polypeptide is also
XX CC useful for identifying compounds that binds to a naturally processed
XX CC class I or class II MHC-binding polypeptide. The polypeptides and
XX CC polynucleotides are particularly useful for treating or preventing
XX CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
XX CC lymphoma or leukaemia. These are also useful for screening agents for
XX CC treating the above mentioned diseases. This sequence represents an
XX CC expressed protein tag (EPT) isolated from human tissue for translational
XX CC profiling. Note: This sequence does not appear in the printed
XX CC specification but was obtained in electronic format directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 9 AA;
Query Match 100.0%; Score 44; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. NO. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KVAELVHFL 9
Db 1 KVAELVHFL 9
RESULT 22
ABU03321
ID ABU03321 standard; protein; 9 AA.
XX AC ABU03321;
XX DT 29-JAN-2003 (first entry)

XX DE Human expressed protein tag (EPT) #101.
XX KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
XX KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX OS Homo sapiens.
XX PN WO200278524-A2.
XX PD 10-OCT-2002.
XX PF 28-MAR-2002; 2002WO-US009671.
XX PR 28-MAR-2001; 2001US-0279495P.
XX PR 21-MAY-2001; 2001US-0292544P.
XX PR 08-AUG-2001; 2001US-0310801P.
XX PR 01-OCT-2001; 2001US-0326370P.
XX PR 04-DEC-2001; 2001US-0336780P.
XX PR 20-FEB-2002; 2002US-0358985P.
XX PA (ZYCO-) ZYCOS INC.
XX PI Chicx RM, Tomlinson AJ, Urban RG;
XX DR WPI; 2003-040607/03.
XX PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX PT cytoskeletal proteins, receptors or transcription factors), useful for
XX PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
XX PT leukemia.
XX PS Claim 10; SEQ ID NO 101; 134pp; English.
XX CC The invention describes a purified polypeptide, which comprises a
XX CC fragment of a kinase, phosphatase, protease, protease inhibitor,
XX CC transporter, cytoskeletal protein, receptor or transcription factor. The
XX CC polypeptide is useful as an immunogenic composition for eliciting in a
XX CC mammal an immunogenic response directed against any of the purified
XX CC polypeptide. The purified polypeptide, or the antibody that binds to this
XX CC polypeptide, is useful for treating cancer. The polypeptide is also
XX CC useful for identifying compounds that binds to a naturally processed
XX CC class I or class II MHC-binding polypeptide. The polypeptides and
XX CC polynucleotides are particularly useful for treating or preventing
XX CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
XX CC lymphoma or leukaemia. These are also useful for screening agents for
XX CC treating the above mentioned diseases. This sequence represents an
XX CC expressed protein tag (EPT) isolated from human tissue for translational
XX CC profiling. Note: This sequence does not appear in the printed
XX CC specification but was obtained in electronic format directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 9 AA;
Query Match 100.0%; Score 44; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. NO. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KVAELVHFL 9
Db 1 KVAELVHFL 9
RESULT 23
ABU04427
ID ABU04427 standard; protein; 9 AA.
XX AC ABU04427;
XX DT 29-JAN-2003 (first entry)
```

```
XX DE Human expressed protein tag (EPT) #1093.
XX KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
XX KW protease; protease inhibitor; transporter; cytoskeletal protein;
XX KW receptor; transcription factor; cancer; MHC;
XX KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
XX KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX OS Homo sapiens.
XX PN WO200278524-A2.
XX PD 10-OCT-2002.
XX PF 28-MAR-2002; 2002WO-US009671.
XX PR 28-MAR-2001; 2001US-0279495P.
XX PR 21-MAY-2001; 2001US-0292544P.
XX PR 08-AUG-2001; 2001US-0310801P.
XX PR 01-OCT-2001; 2001US-0326370P.
XX PR 04-DEC-2001; 2001US-0336780P.
XX PR 20-FEB-2002; 2002US-0358985P.
XX PA (ZYCO-) ZYCOS INC.
XX PI Chicx RM, Tomlinson AJ, Urban RG;
XX DR WPI; 2003-040607/03.
XX KW New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX KW cytoskeletal proteins, receptors or transcription factors), useful for
XX KW treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
XX KW leukemia.
XX PS Example 2; SEQ ID NO 1093; 134pp; English.
XX CC The invention describes a purified polypeptide, which comprises a
XX CC fragment of a kinase, phosphatase, protease, protease inhibitor,
XX CC transporter, cytoskeletal protein, receptor or transcription factor. The
XX CC polypeptide is useful as an immunogenic composition for eliciting in a
XX CC mammal an immunogenic response directed against any of the purified
XX CC polypeptide. The purified polypeptide, or the antibody that binds to this
XX CC polypeptide, is useful for treating cancer. The polypeptide is also
XX CC useful for identifying compounds that binds to a naturally processed
XX CC class I or class II MHC-binding polypeptide. The polypeptides and
XX CC polynucleotides are particularly useful for treating or preventing
XX CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
XX CC lymphoma or leukaemia. These are also useful for screening agents for
XX CC treating the above mentioned diseases. This sequence represents an
XX CC expressed protein tag (EPT) isolated from human tissue for translational
XX CC profiling. Note: This sequence does not appear in the printed
XX CC specification but was obtained in electronic format directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 9 AA;
XX Query Match 100.0%; Score 44; DB 6; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 1.4e+06;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 KVAELVHFL 9
XX Db 1 KVAELVHFL 9
XX RESULT 24
XX ABU04435
XX ID ABU04435 standard; protein; 9 AA.
XX AC ABU04435;
XX XX
XX DT 29-JAN-2003 (first entry)

XX DE Human expressed protein tag (EPT) #1101.
XX KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
XX KW protease; protease inhibitor; transporter; cytoskeletal protein;
XX KW receptor; transcription factor; cancer; MHC;
XX KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
XX KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX OS Homo sapiens.
XX PN WO200278524-A2.
XX PD 10-OCT-2002.
XX PF 28-MAR-2002; 2002WO-US009671.
XX PR 28-MAR-2001; 2001US-0279495P.
XX PR 21-MAY-2001; 2001US-0292544P.
XX PR 08-AUG-2001; 2001US-0310801P.
XX PR 01-OCT-2001; 2001US-0326370P.
XX PR 04-DEC-2001; 2001US-0336780P.
XX PR 20-FEB-2002; 2002US-0358985P.
XX PA (ZYCO-) ZYCOS INC.
XX PI Chicx RM, Tomlinson AJ, Urban RG;
XX DR WPI; 2003-040607/03.
XX KW New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX KW cytoskeletal proteins, receptors or transcription factors), useful for
XX KW treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
XX KW leukemia.
XX PS Example 2; SEQ ID NO 1101; 134pp; English.
XX CC The invention describes a purified polypeptide, which comprises a
XX CC fragment of a kinase, phosphatase, protease, protease inhibitor,
XX CC transporter, cytoskeletal protein, receptor or transcription factor. The
XX CC polypeptide is useful as an immunogenic composition for eliciting in a
XX CC mammal an immunogenic response directed against any of the purified
XX CC polypeptide. The purified polypeptide, or the antibody that binds to this
XX CC polypeptide, is useful for treating cancer. The polypeptide is also
XX CC useful for identifying compounds that binds to a naturally processed
XX CC class I or class II MHC-binding polypeptide. The polypeptides and
XX CC polynucleotides are particularly useful for treating or preventing
XX CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
XX CC lymphoma or leukaemia. These are also useful for screening agents for
XX CC treating the above mentioned diseases. This sequence represents an
XX CC expressed protein tag (EPT) isolated from human tissue for translational
XX CC profiling. Note: This sequence does not appear in the printed
XX CC specification but was obtained in electronic format directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 9 AA;
XX Query Match 100.0%; Score 44; DB 6; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 1.4e+06;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 KVAELVHFL 9
XX Db 1 KVAELVHFL 9
XX RESULT 25
XX AAR73850
XX ID AAR73850 standard; peptide; 10 AA.
XX XX
XX AC AAR73850;
XX XX
XX DT 25-MAR-2003 (revised)
```


DT 22-JUN-1995 (first entry)
XX Antigen fragment 166, from MAGE3 has binding affinity for HLA-2.1.
DE antigen; epitope; immunogenic target protein; PSA; HBVC; HBVs; EBV; HIV1;
XX plasma specific antigen; hepatitis B virus; Epstein Barr;
KW human immunodeficiency virus; human papilloma virus; p53; c-ERB2; MAGE-1;
KW melanoma antigen-1; core antigen; surface antigen;
KW pharmaceutical composition; in vivo; ex vivo; therapeutic; diagnostic;
KW MHC class I molecule; major histocompatibility complex; HLA-A2.1; 9mer;
KW 10mer; anchor; human leukocyte antigen; PLP; 8mer; algorithm prediction;
KW MBP; CMV; cytomegalovirus; HSV; herpes simplex virus; influenza A; M1;
KW LCMV.
XX Homo sapiens.
OS
XX WO9420127-A1.
XX 15-SEP-1994.
XX 04-MAR-1994; 94WO-US002353.
XX 05-MAR-1993; 93US-00027146.
PR 04-JUN-1993; 93US-00073205.
PR 29-NOV-1993; 93US-00159184.
XX (CYTE-) CYTEL CORP.
XX Grey HM, Sette A, Sidney J, Kast W;
XX WPI; 1994-302678/37.
XX Immunogenic peptide(s) having an HLA-A2.1 binding motif - used for
PT treatment or prophylaxis of cancer, virus infection or autoimmune
PT diseases.
XX Disclosure; Page 86; 138pp; English.
XX AAR73685-876 are potential peptide binders of HLA-A2.1 motif. Using
CC motifs disclosed in the invention, these peptides were screened for
CC further motifs. Only peptides with binding affinity of at least 1%
CC (binding affinity is expressed as an IC50 value) as compared to the
CC standard peptide (AAR71293) in assays. This peptide from MAGE3 has a
CC binding value of 0.0120. The peptides of the invention can induce
CC cytotoxic T lymphocytes which can react with target cells. They can be
CC used for the treatment or prophylaxis of cancer, eg. prostate cancer or
CC lymphoma, etc. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 10 AA;
SQ
Query Match 100.0%; Score 44; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. NO. 0.028;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KVAELVHFL 9
Db 1 KVAELVHFL 9
RESULT 26
AAW70038
ID AAW70038 standard; peptide; 10 AA.
XX
XX AAW70038;
XX
XX 22-OCT-1998 (first entry)
XX MAGE 3 antigen derived HLA-A2.1 binding peptide 4 (residues 112-121).
XX Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
KW human leukocyte antigen; HLA; tumour associated antigen; cancer;
KW antigen presenting cell; APC; immunogenic peptide; immune disorder;
KW viral infection; AIDS; hepatitis; bacterial infection; malaria;
KW

KW fungal infection; tuberculosis; melanoma; MAGE antigen.
XX Synthetic.
OS Homo sapiens.
XX WO9833888-A1.
XX 06-AUG-1998.
XX 30-JAN-1998; 98WO-US001959.
XX 31-JAN-1997; 97US-0036696P.
XX (EPIM-) EPIMMUNE INC.
XX Teai V, Southwood S, Sidney J, Sette A, Celis E;
XX WPI; 1998-437445/37.
XX Production of antigen-specific cytotoxic T cells - by incubating
PT immunogenic peptide(s) from antigen that binds class I major
PT histocompatibility complex molecules with pre-treated antigen presenting
PT cells.
XX Example 5; Page 72; 104pp; English.
XX Sequences shown in AAW70027 to AAW70043 represent peptides derived from
CC MAGE2 and MAGE3 antigens. The peptides can bind to a human leukocyte
CC antigen (HLA), HLA-A2.1 and are used to exemplify the method of invention
CC of producing antigen-specific cytotoxic T cells (CTLs) in vitro. The
CC method comprises contacting immunogenic peptides from an antigen that
CC binds class I major histocompatibility complex (MHC) molecules with
CC antigen presenting cells (APCs) pretreated with pretreatment growth
CC factors, and incubating the APCs with purified CD8 cells in the presence
CC of at least 2 incubation growth factors, thereby producing antigen-
CC specific CTLs. A method for specifically killing target cells in a human
CC patient is also provided which comprises obtaining a fluid sample
CC containing CTLs from a patient, contacting the cytotoxic T cells with
CC APCs pretreated with pre-treatment growth factors, where the APCs
CC comprise class I MHC molecules. The pretreated APCs are incubated with
CC the cytotoxic growth factors, thereby producing activated CTLs which are
CC contacted with a carrier to form a composition. The composition can then
CC be administered to the patient. The activated CTLs can be used for
CC treating cancers, immune disorders, viral infections, AIDS, hepatitis,
CC bacterial infection, fungal infection, malaria or tuberculosis
XX Sequence 10 AA;
SQ
Query Match 100.0%; Score 44; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. NO. 0.028;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KVAELVHFL 9
Db 1 KVAELVHFL 9
RESULT 27
AAW47162
ID AAW47162 standard; peptide; 10 AA.
XX
XX AAW47162;
XX
XX 01-DEC-1999 (first entry)
XX Immunogenic peptide having a human leukocyte antigen binding motif #1773.
XX Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
KW immune response; T cell activation; major histocompatibility complex;
KW cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;
KW prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
KW vaccine; immunisation.
KW

XX PA (EPIM-) EPIMUNE INC.
XX PI Fikes J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E;
XX PI Keogh E;
XX DR WPI; 2001-375002/39.
XX XX
PT An isolated prepared MAGE2/3 epitope (I) for use in pharmaceuticals for
XX the treatment and prevention of cancer.
XX PS Claim 1; Page 160; 171pp; English.
XX XX
CC The present invention describes MAGE2/3 epitopes (I). Also described are:
CC (1) a clonal cytotoxic T lymphocyte (CTL) that is cultured in vivo and
CC binds to a complex of (I); (2) a peptide (II) comprising (I) and a second
CC epitope and has less than 50 contiguous amino acids; (3) a vaccine
CC composition comprising (II), a unit dose of a peptide with at least 50
CC contiguous amino acids with 100% identity to the native peptide sequence
CC of MAGE2/3, and a pharmaceutical excipient; (4) an isolated nucleic acid
CC encoding (I); and (5) an isolated nucleic acid encoding (II). (I) has
CC cytotoxic activity, and can be used in vaccines and as an
CC immunostimulant. A vaccine of (3) is useful for the treatment and
CC prevention of cancer. (I) is useful for monitoring or evaluating an
CC immune response by incubating a T-lymphocyte sample from a patient with
CC (I) that binds to an human leukocyte antigen (HLA) allele present in the
CC patient and detecting the presence of the T-lymphocyte that binds to the
CC peptide. The vaccine allows the opportunity to combine epitopes derived
CC from multiple tumour-associated molecules reducing the likelihood of
CC tumour escape due to antigen loss. AAG84515 to AAG84909 and AAB99725
CC represent amino acid sequences used in the exemplification of the present
CC invention
XX SQ Sequence 10 AA;

Query Match 100.0%; Score 44; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVAELVHFL 9
| | | | |
Db 1 KVAELVHFL 9

RESULT 30
ABU04436
ID ABU04436 standard; protein; 10 AA.

XX AC ABU04436;

XX DT 29-JAN-2003 (first entry)

XX DE Human expressed protein tag (EPT) #1102.

XX KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

XX OS Homo sapiens.

XX PN WO200278524-A2.

XX PD 10-OCT-2002.

XX PF 28-MAR-2002; 2002WO-US009671.

XX XX 28-MAR-2001; 2001US-0279495P.

PR 21-MAY-2001; 2001US-0292544P.

PR 08-AUG-2001; 2001US-0310801P.

PR 01-OCT-2001; 2001US-0326370P.

PR 04-DEC-2001; 2001US-0336780P.

PR 20-FEB-2002; 2002US-0358985P.

XX PA (ZYCO-) ZYCOS INC.

XX PI Chicz RM, Tomlinson AJ, Urban RG;

XX DR WPI; 2003-040607/03.

XX XX
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.

XX XX Example 2; SEQ ID NO 1102; 134pp; English.

XX CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 10 AA;

Query Match 100.0%; Score 44; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVAELVHFL 9
| | | | |
Db 1 KVAELVHFL 9

RESULT 31

ABU04442
ID ABU04442 standard; protein; 10 AA.

XX AC ABU04442;

XX DT 29-JAN-2003 (first entry)

XX DE Human expressed protein tag (EPT) #1108.

XX KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

XX OS Homo sapiens.

XX PN WO200278524-A2.

XX PD 10-OCT-2002.

XX PF 28-MAR-2002; 2002WO-US009671.

XX XX 28-MAR-2001; 2001US-0279495P.

PR 21-MAY-2001; 2001US-0292544P.

PR 08-AUG-2001; 2001US-0310801P.

PR 01-OCT-2001; 2001US-0326370P.

PR 04-DEC-2001; 2001US-0336780P.

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PR 20-FEB-2002; 2002US-0358985P.
XX (ZYCO-) ZYCOS INC.
XX
XX Chicx RM, Tomlinson AJ, Urban RG;
XX WPI; 2003-040607/03.
XX
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
XX Example 2; SEQ ID NO 1108; 134pp; English.
XX
XX The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 10 AA;

Query Match 100.0%; Score 44; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVAELVHFL 9
DB 1 KVAELVHFL 9

RESULT 32
ABU04450
ID ABU04450 standard; protein; 10 AA.
XX
XX ABU04450;
XX
XX 29-JAN-2003 (first entry)
XX
XX Human expressed protein tag (EPT) #1116.
XX
XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
XX Homo sapiens.
XX
XX WO200278524-A2.
XX
XX 10-OCT-2002.
XX
XX 28-MAR-2002; 2002WO-US009671.
XX
XX 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.

PR 20-FEB-2002; 2002US-0358985P.
XX (ZYCO-) ZYCOS INC.
XX
XX Chicx RM, Tomlinson AJ, Urban RG;
XX WPI; 2003-040607/03.
XX
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
XX Example 2; SEQ ID NO 1116; 134pp; English.
XX
XX The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 10 AA;

Query Match 100.0%; Score 44; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVAELVHFL 9
DB 1 KVAELVHFL 9

RESULT 33
ABU04438
ID ABU04438 standard; protein; 10 AA.
XX
XX ABU04438;
XX
XX 29-JAN-2003 (first entry)
XX
XX Human expressed protein tag (EPT) #1104.
XX
XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
XX Homo sapiens.
XX
XX WO200278524-A2.
XX
XX 10-OCT-2002.
XX
XX 28-MAR-2002; 2002WO-US009671.
XX
XX 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.

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PR 20-FEB-2002; 2002US-0358985P.
XX (ZYCO-) ZYCOS INC.
XX Chicx RM, Tomlinson AJ, Urban RG;
XX WPI; 2003-040607/03.
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
XX Example 2; SEQ ID NO 1104; 134pp; English.
XX
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 10 AA;
XX
Query Match 100.0%; Score 44; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KVAELVHFL 9
DB 1 KVAELVHFL 9
RESULT 34
ABU04443
ID ABU04443 standard; protein; 10 AA.
XX
AC ABU04443;
XX
XX 29-JAN-2003 (first entry)
XX
XX Human expressed protein tag (EPT) #1109.
XX
XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
XX Homo sapiens.
XX
XX WO200278524-A2.
XX
XX 10-OCT-2002.
XX
XX 28-MAR-2002; 2002WO-US009671.
XX
XX 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR
PR 20-FEB-2002; 2002US-0358985P.
XX (ZYCO-) ZYCOS INC.
XX Chicx RM, Tomlinson AJ, Urban RG;
XX WPI; 2003-040607/03.
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
XX Example 2; SEQ ID NO 1109; 134pp; English.
XX
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 10 AA;
XX
Query Match 100.0%; Score 44; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KVAELVHFL 9
DB 1 KVAELVHFL 9
RESULT 35
AAB08828
ID AAB08828 standard; peptide; 15 AA.
XX
AC AAB08828;
XX
XX 02-JAN-2001 (first entry)
XX
XX Amino acid sequence of a MAGE-3 derived immunogenic peptide.
XX
XX Melanoma associated antigen-3; MAGE-3; immunogenic peptide;
KW major histocompatibility complex; MHC; class II molecule; tumour;
KW CD4+ T cell proliferation; melanoma cell; immune response; vaccine.
XX
XX Homo sapiens.
XX
XX WO200052045-A2.
XX
XX 08-SEP-2000.
XX
XX 23-FEB-2000; 2000WO-EP001458.
XX
XX 26-FEB-1999; 99IT-MI000396.
XX
XX (SANR-) FOND CENT SAN RAFFAELE DEL MONTE TABOR.
XX
XX Protti MP, Dellabona P;
XX
XX WPI; 2000-601867/57.
```

XX Novel melanoma associated antigen (MAGE)-3 derived immunogenic peptides
PT useful as vaccine for inducing immune response against tumor.
XX
PS Claim 1; Page 18; 27pp; English.
XX
CC AAB0827-37 represent melanoma associated antigen (MAGE)-3 derived
CC immunogenic peptides. The peptides are capable of binding to major
CC histocompatibility complex (MHC) class II molecules. Stimulation with the
CC peptides induces proliferation of CD4+ T cells, and of their cytolytic
CC activity. CD4+ T cells exposed to the peptides were able to cause lysis
CC of melanoma cells expressing MAGE-3 and HLA-DR molecules. The peptides
CC are useful for inducing an immune response against tumour cells
CC expressing a MAGE-3 antigen. They are also useful for the preparation of
CC anti-tumour medicament for use as a vaccine
XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 44; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVAELVHFL 9
Db 2 KVAELVHFL 10

RESULT 36
AAG84626
ID AAG84626 standard; peptide; 15 AA.
XX
AC AAG84626;
XX
DT 10-SEP-2001 (first entry)
XX
DE MAGE3 DR supermotif binding peptide #37.
XX
KW Human; human leukocyte antigen; HLA epitope; cytotoxic T lymphocyte; CTL;
KW MAGE2; MAGE3; melanoma antigen gene; immune response; vaccine; cancer;
KW cytosstatic; immunostimulant.
XX
OS Homo sapiens.
OS Synthetic.
XX
FN WO200142267-A1.
XX
PD 14-JUN-2001.
XX
PP 11-DEC-2000; 2000WO-US033545.
XX
PR 10-DEC-1999; 99US-00458298.
XX
PA (EPIM-) EPIMMUNE INC.
XX
PI Fikes J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E;
PI Keogh E;
XX
DR WPI; 2001-375002/39.
XX
PT An isolated prepared MAGE2/3 epitope (I) for use in pharmaceuticals for
PT the treatment and prevention of cancer.
XX
PS Disclosure; Page 138; 171pp; English.
XX
CC The present invention describes MAGE2/3 epitopes (I). Also described are:
CC (1) a clonal cytotoxic T lymphocyte (CTL) that is cultured in vivo and
CC binds to a complex of (I); (2) a peptide (II) comprising (I) and a second
CC epitope and has less than 50 contiguous amino acids; (3) a vaccine
CC composition comprising (II), a unit dose of a peptide with at least 50
CC contiguous amino acids with 100% identity to the native peptide sequence
CC of MAGE2/3, and a pharmaceutical excipient; (4) an isolated nucleic acid
CC encoding (I); and (5) an isolated nucleic acid encoding (II). (I) has
CC cytostatic activity, and can be used in vaccines and as an

CC immunostimulant. A vaccine of (3) is useful for the treatment and
CC prevention of cancer. (I) is useful for monitoring or evaluating an
CC immune response by incubating a T-lymphocyte sample from a patient with
CC (I) that binds to an human leukocyte antigen (HLA) allele present in the
CC patient and detecting the presence of the T-lymphocyte that binds to the
CC peptide. The vaccine allows the opportunity to combine epitopes derived
CC from multiple tumour-associated molecules reducing the likelihood of
CC tumour escape due to antigen loss. AAG84515 to AAG84909 and AAB99725
CC represent amino acid sequences used in the exemplification of the present
XX invention
SQ Sequence 15 AA;

Query Match 100.0%; Score 44; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVAELVHFL 9
Db 7 KVAELVHFL 15

RESULT 37
ABU04426
ID ABU04426 standard; protein; 15 AA.
XX
AC ABU04426;
XX
DT 29-JAN-2003 (first entry)
XX
DE Human expressed protein tag (EPT) #1092.
XX
KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
OS Homo sapiens.
XX
PN WO200278524-A2.
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-US009671.
XX
PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
PA (ZYCO-) ZYCOS INC.
XX
PI Chicx RM, Tomlinson AJ, Urban RG;
XX
DR WPI; 2003-040607/03.
XX
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
PS Example 2; SEQ ID NO 1092; 134pp; English.
XX
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also

CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 15 AA;

Query Match 100.0%; Score 44; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVAELVHFL 9
| | | | |
DB 2 KVAELVHFL 10

RESULT 38
ABU04434
ID ABU04434 standard; protein; 15 AA.
XX
AC ABU04434;
XX
XX 29-JAN-2003 (first entry)
XX
XX Human expressed protein tag (EPT) #1100.

XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

XX Homo sapiens.

XX WO200278524-A2.

XX 10-OCT-2002.

XX 28-MAR-2002; 2002WO-US009671.

XX 28-MAR-2001; 2001US-0279495P.

XX 21-MAY-2001; 2001US-0292544P.

XX 08-AUG-2001; 2001US-0310801P.

XX 01-OCT-2001; 2001US-0326370P.

XX 04-DEC-2001; 2001US-0336780P.

XX 20-FEB-2002; 2002US-0358985P.

XX (ZYCO-) ZYCO INC.

XX Chicx RM, Tomlinson AJ, Urban RG;

XX WPI; 2003-040607/03.

XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX cytoskeletal proteins, receptors or transcription factors), useful for
XX treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
XX leukemia.

XX Example 2; SEQ ID NO 1100; 134pp; English.

XX The invention describes a purified polypeptide, which comprises a
XX fragment of a kinase, phosphatase, protease, protease inhibitor,
XX transporter, cytoskeletal protein, receptor or transcription factor. The
XX polypeptide is useful as an immunogenic composition for eliciting in a
XX mammal an immunogenic response directed against any of the purified
XX polypeptide. The purified polypeptide, or the antibody that binds to this
XX polypeptide, is useful for treating cancer. The polypeptide is also

CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 15 AA;

Query Match 100.0%; Score 44; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVAELVHFL 9
| | | | |
DB 7 KVAELVHFL 15

RESULT 39
AAV01721
ID AAV01721 standard; peptide; 16 AA.
XX
AC AAV01721;
XX
XX 25-JUN-1999 (first entry)
XX
XX Peptide derived from MAGE-3 protein amino acids 111-126.

XX MAGE-3 tumour associated gene; human leucocyte antigen Class II;
KW autologous CD4+ cell; MAGE-3 related disease; cancer; melanoma;
KW osteosarcoma; leukemia; carcinoma.

OS Synthetic.

OS Homo sapiens.

XX WO9914326-A1.

XX 25-MAR-1999.

XX 04-SEP-1998; 98WO-US018601.

XX 12-SEP-1997; 97US-00928615.

XX (LUDW-) LUDWIG INST CANCER RES.

XX (UYVR-) UNIV VRIJE BRUSSEL.

XX Thielemans K, Heirman C, Corthals J, Chaux P, Stroobant V;

XX Boon-Falleur T, Van Der Bruggen P, Luiten R;

XX WPI; 1999-244031/20.

XX Isolated peptides that bind to human leucocyte antigen class II
XX molecules.

XX Claim 3; Page 36; 88pp; English.

XX The present sequence represents a peptide derived from the MAGE-3
XX protein. This protein is encoded by the MAGE-3 tumour associated gene.
XX Peptides (AAV01721-25) that bind human leucocyte antigen (HLA) Class II
XX molecules can be derived from the MAGE-3 protein. These peptides and
XX autologous CD4+ cells that bind to a complex of MAGE-3 peptide and HLA
XX Class II, are used to treat MAGE-3 related diseases, particularly cancers
XX (e.g. melanoma, osteosarcoma, leukemia and various forms of carcinoma).
XX The peptides are also used to produce specific antibodies. Detection of
XX of the peptides, e.g. in binding assays, particularly with antibodies, is
XX used for diagnosis of such diseases

XX Sequence 16 AA;

Query Match 100.0%; Score 44; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.046;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KVAELVHFL 9
Db 2 KVAELVHFL 10

RESULT 40

AA92313
ID AA92313 standard; peptide; 16 AA.

XX AC AA92313;

XX DT 10-AUG-2000 (first entry)

XX DE MAGE-A3 antigenic peptide epitope.

XX KW MAGE-A3; antigen; epitope; cytotoxic T lymphocyte; CTL; complex; HLA;
XX KW human leukocyte antigen.

XX OS Homo sapiens.

XX FN WO200020445-A2.

XX PD 13-APR-2000.

XX PF 15-SEP-1999; 99WO-IB001664.

XX PR 02-OCT-1998; 98US-00165863.

XX PR 09-APR-1999; 99US-00289350.

XX PA (CHAU//) CHAUX P.

XX PA (LUIT//) LUITEN R.

XX PA (DEMO//) DEMOTIE N.

XX PA (DUFF//) DUFFOUR M.

XX PA (LURQ//) LURQUIN C.

XX PA (TRAV//) TRAVERSARI C.

XX PA (STRO//) STROOBANT V.

XX PA (CORN//) CORNELIS G R.

XX PA (BOON//) BOON-FALLEUR T.

XX PA (VERU//) VAN DER BRUGGEN P.

XX PA (SCHU//) SCHULTZ E.

XX PA (WARN//) WARNIER G.

PI Chaux P, Luiten R, Demotte N, Duffour M, Lurquin C, Traversari C;

PI Stroobant V, Cornelis GR, Boon-Falleur T, Van Der Bruggen P;

PI Schultz E, Warnier G;

XX WPI; 2000-303739/26.

XX Isolation of cytotoxic T-lymphocytes clones by successive steps of
XX stimulation and testing of lymphocytes with antigen presenting cells
XX which present antigens derived from different expression systems.

XX Example 12; Page 71; 99pp; English.

XX A novel method of isolation of cytotoxic T-lymphocytes (CTL) clones
XX comprises successive steps of stimulation and testing of lymphocytes with
XX antigen presenting cells (APCs) which present antigens derived from
XX different expression systems. The CTL clones isolated recognize specific
XX antigenic peptides of proteins, preferably of the MAGE family. The APC is
XX autologous and each expression system is different from at least one of
XX the other expression systems, therefore isolating a cytotoxic T cell
XX clone specific for the protein. The method can also be used to identify
XX an antigenic peptide epitope. Isolated CTL clones specific for a
XX peptide/human leukocyte antigen (HLA) complex are claimed. The CTL cells
XX specific for the complexes, peptides or cells which present the complexes
XX on the cell surface are useful for treating pathological conditions
XX characterized by abnormal expression of the complexes

XX Sequence 16 AA;

9

Query Match 100.0%; Score 44; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.046;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KVAELVHFL 9
Db 6 KVAELVHFL 14

Search completed: July 23, 2004, 12:51:37
Job time : 53 secs

Result No.	Score	Query Match	Length	DB	ID	Description	
1	44	100.0	9	3	US-09-183-931-34	Sequence 34, Appl	
2	44	100.0	9	4	US-09-705-160-34	Sequence 34, Appl	
3	44	100.0	9	4	US-09-543-608A-5	Sequence 5, Appl	
4	44	100.0	16	2	US-08-928-615-3	Sequence 3, Appl	
5	44	100.0	16	3	US-09-166-448-3	Sequence 3, Appl	
6	44	100.0	16	4	US-09-348-933-3	Sequence 3, Appl	
7	44	100.0	16	4	US-09-697-884-3	Sequence 3, Appl	
8	44	100.0	314	4	US-08-928-615-2	Sequence 2, Appl	
9	44	100.0	314	3	US-09-166-448-2	Sequence 2, Appl	
10	44	100.0	314	4	US-09-348-933-2	Sequence 2, Appl	
11	44	100.0	314	4	US-09-697-884-2	Sequence 2, Appl	
12	44	100.0	314	4	US-09-392-714-30	Sequence 30, Appl	
13	40	90.9	9	4	US-08-197-484-86	Sequence 86, Appl	
14	40	90.9	9	4	US-08-197-484-145	Sequence 145, Appl	
15	40	90.9	9	5	PCT-US95-02131-86	Sequence 86, Appl	
16	40	90.9	9	5	PCT-US95-02121-145	Sequence 145, Appl	
17	40	90.9	129	4	US-09-634-238-358	Sequence 358, Appl	
18	39	88.6	14	3	US-09-166-448-26	Sequence 26, Appl	
19	39	88.6	14	4	US-09-697-884-26	Sequence 26, Appl	
20	39	88.6	15	3	US-09-166-448-25	Sequence 25, Appl	
21	39	88.6	15	4	US-09-697-884-25	Sequence 25, Appl	
22	39	88.6	16	3	US-09-166-448-24	Sequence 24, Appl	
23	39	88.6	16	4	US-09-697-884-24	Sequence 24, Appl	
24	37	84.1	9	1	US-08-217-188A-3	Sequence 3, Appl	
25	37	84.1	9	1	US-08-687-226-3	Sequence 3, Appl	
26	37	84.1	9	3	US-08-667-725B-3	Sequence 3, Appl	
27	37	84.1	9	3	US-09-007-748-3	Sequence 3, Appl	

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; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION:
US-09-705-160-34

Query Match      100.0%; Score 44; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVAELVHFL 9
Db 1 KVAELVHFL 9

RESULT 3
US-09-543-608A-5
; Sequence 5, Application US/09543608A
; Patent No. 6602510
; GENERAL INFORMATION:
; APPLICANT: Fikes, John D.
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa A.
; APPLICANT: Chesnut, Robert
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: HLA Class I A2 Tumor Associated Antigen
; FILE REFERENCE: Peptides and Vaccine Compositions
; FILE REFERENCE: 018623-015710US
; CURRENT APPLICATION NUMBER: US/09/543,608A
; CURRENT FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MAGE3.112
US-09-543-608A-5

Query Match      100.0%; Score 44; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVAELVHFL 9
Db 1 KVAELVHFL 9

RESULT 4
US-08-928-615-3
; Sequence 3, Application US/08928615
; Patent No. 5965535
; GENERAL INFORMATION:
; APPLICANT: Chauv, Pascal
; APPLICANT: Stroobant, Vincent
; APPLICANT: Boon, Thierry
; APPLICANT: van der Bruggen, Pierre
; TITLE OF INVENTION: MAGE-3 PEPTIDES PRESENTED
; TITLE OF INVENTION: BY HLA CLASS II MOLECULES
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02210-2211
; COMPUTER READABLE FORM:

; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION:
US-09-705-160-34

Query Match      100.0%; Score 44; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVAELVHFL 9
Db 1 KVAELVHFL 9

RESULT 3
US-09-543-608A-5
; Sequence 5, Application US/09543608A
; Patent No. 6602510
; GENERAL INFORMATION:
; APPLICANT: Fikes, John D.
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa A.
; APPLICANT: Chesnut, Robert
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: HLA Class I A2 Tumor Associated Antigen
; FILE REFERENCE: Peptides and Vaccine Compositions
; FILE REFERENCE: 018623-015710US
; CURRENT APPLICATION NUMBER: US/09/543,608A
; CURRENT FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MAGE3.112
US-09-543-608A-5

Query Match      100.0%; Score 44; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVAELVHFL 9
Db 1 KVAELVHFL 9

RESULT 4
US-08-928-615-3
; Sequence 3, Application US/08928615
; Patent No. 5965535
; GENERAL INFORMATION:
; APPLICANT: Chauv, Pascal
; APPLICANT: Stroobant, Vincent
; APPLICANT: Boon, Thierry
; APPLICANT: van der Bruggen, Pierre
; TITLE OF INVENTION: MAGE-3 PEPTIDES PRESENTED
; TITLE OF INVENTION: BY HLA CLASS II MOLECULES
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02210-2211
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/928,615
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Van Amsterdam, John R.
; REGISTRATION NUMBER: 40,212
; REFERENCE/DOCKET NUMBER: L0461/7017
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-928-615-3

Query Match      100.0%; Score 44; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVAELVHFL 9
Db 2 KVAELVHFL 10

RESULT 5
US-09-166-448-3
; Sequence 3, Application US/09166448
; Patent No. 6291430
; GENERAL INFORMATION:
; APPLICANT: Chauv, Pascal
; APPLICANT: Vantomme, Valrie
; APPLICANT: Stroobant, Vincent
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Thielemans, Kris
; APPLICANT: Corthals, Jurgen
; TITLE OF INVENTION: MAGE-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES
; FILE REFERENCE: L0461/7052
; CURRENT APPLICATION NUMBER: US/09/166,448
; CURRENT FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-166-448-3

Query Match      100.0%; Score 44; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVAELVHFL 9
Db 2 KVAELVHFL 10

RESULT 6
US-09-348-933-3
; Sequence 3, Application US/09348933
; Patent No. 6369211
; GENERAL INFORMATION:
; APPLICANT: Chauv, Pascal
; APPLICANT: Stroobant, Vincent
```

```
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: van der Bruggen, Pierre
; TITLE OF INVENTION: MAGE-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES
; FILE REFERENCE: L0461/7065
; CURRENT APPLICATION NUMBER: US/09/348,933
; CURRENT FILING DATE: 1999-07-07
; EARLIER APPLICATION NUMBER: US 08/928,615
; EARLIER FILING DATE: 1997-09-12
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-348-933-3

Query Match      100.0%; Score 44; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVAELVHFL 9
       1|1|1|1|1|1|
Db      2 KVAELVHFL 10

RESULT 7
US-09-697-884-3
; Sequence 3, Application US/09697884
; Patent No. 6426217
; GENERAL INFORMATION:
; APPLICANT: Chauv, Pascal
; APPLICANT: Vantomme, Valrie
; APPLICANT: Stroobant, Vincent
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Thielemans, Kris
; APPLICANT: Corthals, Jorgen
; TITLE OF INVENTION: MAGE-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES
; FILE REFERENCE: L0461/7052
; CURRENT APPLICATION NUMBER: US/09/697,884
; CURRENT FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: 09/166,448
; PRIOR FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-697-884-3

Query Match      100.0%; Score 44; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVAELVHFL 9
       1|1|1|1|1|1|
Db      2 KVAELVHFL 10

RESULT 8
US-08-928-615-2
; Sequence 2, Application US/08928615
; Patent No. 5965535
; GENERAL INFORMATION:
; APPLICANT: Chauv, Pascal
; APPLICANT: Stroobant, Vincent
; APPLICANT: Boon, Thierry
; APPLICANT: van der Bruggen, Pierre
; TITLE OF INVENTION: MAGE-3 PEPTIDES PRESENTED
; BY HLA CLASS II MOLECULES
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:

; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: van der Bruggen, Pierre
; TITLE OF INVENTION: MAGE-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES
; FILE REFERENCE: L0461/7065
; CURRENT APPLICATION NUMBER: US/09/348,933
; CURRENT FILING DATE: 1999-07-07
; EARLIER APPLICATION NUMBER: US 08/928,615
; EARLIER FILING DATE: 1997-09-12
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-348-933-3

Query Match      100.0%; Score 44; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVAELVHFL 9
       1|1|1|1|1|1|
Db      2 KVAELVHFL 10

RESULT 9
US-09-166-448-2
; Sequence 2, Application US/09166448
; Patent No. 6291430
; GENERAL INFORMATION:
; APPLICANT: Chauv, Pascal
; APPLICANT: Vantomme, Valrie
; APPLICANT: Stroobant, Vincent
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Thielemans, Kris
; APPLICANT: Corthals, Jorgen
; TITLE OF INVENTION: MAGE-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES
; FILE REFERENCE: L0461/7052
; CURRENT APPLICATION NUMBER: US/09/166,448
; CURRENT FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-166-448-2

Query Match      100.0%; Score 44; DB 3; Length 314;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVAELVHFL 9
       1|1|1|1|1|1|
Db      112 KVAELVHFL 120
```

```
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02210-2211
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/928,615
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Van Amsterdam, John R.
; REGISTRATION NUMBER: 40,212
; REFERENCE/DOCKET NUMBER: L0461/7017
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 314 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-928-615-2

Query Match      100.0%; Score 44; DB 2; Length 314;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVAELVHFL 9
       1|1|1|1|1|1|
Db      112 KVAELVHFL 120

RESULT 9
US-09-166-448-2
; Sequence 2, Application US/09166448
; Patent No. 6291430
; GENERAL INFORMATION:
; APPLICANT: Chauv, Pascal
; APPLICANT: Vantomme, Valrie
; APPLICANT: Stroobant, Vincent
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Thielemans, Kris
; APPLICANT: Corthals, Jorgen
; TITLE OF INVENTION: MAGE-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES
; FILE REFERENCE: L0461/7052
; CURRENT APPLICATION NUMBER: US/09/166,448
; CURRENT FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-166-448-2

Query Match      100.0%; Score 44; DB 3; Length 314;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVAELVHFL 9
       1|1|1|1|1|1|
Db      112 KVAELVHFL 120
```

```
RESULT 10
US-09-348-933-2
; Sequence 2, Application US/09348933
; Patent No. 6369211
; GENERAL INFORMATION:
; APPLICANT: Chaux, Pascal
; APPLICANT: Stroobant, Vincent
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: van der Bruggen, Pierre
; TITLE OF INVENTION: MAGE-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES
; FILE REFERENCE: L0461/7065
; CURRENT APPLICATION NUMBER: US/09/348,933
; CURRENT FILING DATE: 1999-07-07
; EARLIER APPLICATION NUMBER: US 08/928,615
; EARLIER FILING DATE: 1997-09-12
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-348-933-2

Query Match 100.0%; Score 44; DB 4; Length 314;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVAELVHFL 9
Db 112 KVAELVHFL 120

RESULT 11
US-09-697-884-2
; Sequence 2, Application US/09697884
; Patent No. 6426217
; GENERAL INFORMATION:
; APPLICANT: Chaux, Pascal
; APPLICANT: Vantomme, Val,rie
; APPLICANT: Stroobant, Vincent
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Thielemans, Kris
; APPLICANT: Corthals, Jurgen
; TITLE OF INVENTION: MAGE-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES
; FILE REFERENCE: L0461/7052
; CURRENT APPLICATION NUMBER: US/09/697,884
; CURRENT FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: 09/166,448
; PRIOR FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-697-884-2

Query Match 100.0%; Score 44; DB 4; Length 314;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVAELVHFL 9
Db 112 KVAELVHFL 120

RESULT 12
US-09-392-714-30
; Sequence 30, Application US/09392714A
; Patent No. 6686147
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew J.
```

```
; APPLICANT: Gure, Ali O.
; APPLICANT: Williamson, Barbara
; APPLICANT: Chen, Yao-Tseng
; APPLICANT: Old, Lloyd J.
; TITLE OF INVENTION: Cancer Associated Antigens and Uses
; FILE REFERENCE: L0461/7062
; CURRENT APPLICATION NUMBER: US/09/392,714A
; CURRENT FILING DATE: 1999-09-09
; EARLIER APPLICATION NUMBER: PCT/US98/14679
; EARLIER FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-392-714-30

Query Match 100.0%; Score 44; DB 4; Length 314;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVAELVHFL 9
Db 112 KVAELVHFL 120

RESULT 13
US-08-197-484-86
; Sequence 86, Application US/08197484
; Patent No. 641931
; GENERAL INFORMATION:
; APPLICANT: VITIELLO, Maria A.
; APPLICANT: CHESTNUT, Robert W.
; APPLICANT: SETTE, Alessandro D.
; APPLICANT: CELIS, Esteban
; APPLICANT: GRAY, Howard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
; TITLE OF INVENTION: CTL IMMUNITY
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/197,484
; FILING DATE: 16-FEB-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/935,811
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/874,491
; FILING DATE: 27-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,682
; FILING DATE: 29-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/749,568
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 14137-26-4
```

TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 467-9600
TELEFAX: (206) 623-6793
INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-197-484-86

Query Match 90.9%; Score 40; DB 4; Length 9;
Best Local Similarity 88.9%; Pred. No. 3e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVAELVHFL 9
Db 1 KVAEFVHFL 9

RESULT 14

US-08-197-484-145
Sequence 145, Application US/08197484
Patent No. 641931
GENERAL INFORMATION:
APPLICANT: VITIELLO, Maria A.
APPLICANT: CHESTNUT, Robert W.
APPLICANT: SETTE, Alessandro D.
APPLICANT: CELIS, Esteban
APPLICANT: GRAY, Howard
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
TITLE OF INVENTION: CTL IMMUNITY
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: Steuart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
COUNTRY: US
ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/197,484
FILING DATE: 16-FEB-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/935,811
FILING DATE: 26-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/874,491
FILING DATE: 27-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,682
FILING DATE: 29-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/749,568
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 14137-26-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 467-9600
TELEFAX: (206) 623-6793
INFORMATION FOR SEQ ID NO: 145:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid

STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-197-484-145

Query Match 90.9%; Score 40; DB 4; Length 9;
Best Local Similarity 88.9%; Pred. No. 3e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVAELVHFL 9
Db 1 KVAEFVHFL 9

RESULT 15

PCT-US95-02121-86
Sequence 86, Application PC/TUS9502121
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
TITLE OF INVENTION: CTL IMMUNITY
NUMBER OF SEQUENCES: 153
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/02121
FILING DATE: 16-FEB-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/197,484
FILING DATE: 16-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/935,811
FILING DATE: 26-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/874,491
FILING DATE: 27-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,682
FILING DATE: 29-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/749,568
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 14137-26-4PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 467-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
PCT-US95-02121-86

Query Match 90.9%; Score 40; DB 5; Length 9;
Best Local Similarity 88.9%; Pred. No. 3e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVAELVHFL 9
Db 1 KVAEFVHFL 9

RESULT 16

PCT-US95-02121-145

; Sequence 145, Application PC/TUS9502121
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
; TITLE OF INVENTION: CTL IMMUNITY
; NUMBER OF SEQUENCES: 153
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/02121
; FILING DATE: 16-FEB-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/197,484
; FILING DATE: 16-FEB-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/935,811
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/874,491
; FILING DATE: 27-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,682
; FILING DATE: 29-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/749,568
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 14137-26-4PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 145:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; PCT-US95-02121-145

Query Match 90.9%; Score 40; DB 5; Length 9;
Best Local Similarity 88.9%; Pred. No. 3e+05; Length 9;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVAELVHFL 9
Db 1 KVAELVHFL 9
|||||

RESULT 17
US-09-634-238-358
; Sequence 358, Application US/09634238
; Patent No. 654472
; GENERAL INFORMATION:
; APPLICANT: Glenn, Matthew
; APPLICANT: Havukkala, Ilkka J.
; APPLICANT: Bloksberg, Leonard, N.
; APPLICANT: Lubbers, Mark W.
; APPLICANT: Dekker, James
; APPLICANT: Christensen, Anna C.
; APPLICANT: Holland, Ross
; APPLICANT: O'Toole, Paul W.
; APPLICANT: Reid, Julian R.
; APPLICANT: Coolbear, Timothy
; TITLE OF INVENTION: Polynucleotides, materials incorporating
; TITLE OF INVENTION: them and methods for using them.
; FILE REFERENCE: 11000.1043U1

; CURRENT APPLICATION NUMBER: US/09/634,238
; CURRENT FILING DATE: 2000-08-08
; NUMBER OF SEQ ID NOS: 422
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 358
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Lactobacillus rhamnosus
US-09-634-238-358

Query Match 90.9%; Score 40; DB 4; Length 129;
Best Local Similarity 100.0%; Pred. No. 0.81; Length 129;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVAELVHF 8
Db 103 KVAELVHF 110
|||||

RESULT 18
US-09-166-448-26
; Sequence 26, Application US/09166448
; Patent No. 6291430
; GENERAL INFORMATION:
; APPLICANT: Chau, Pascal
; APPLICANT: Vantomme, Valrie
; APPLICANT: Stroobant, Vincent
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Thielemans, Kris
; APPLICANT: Corthals, Jurgen
; TITLE OF INVENTION: MAGE-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES
; FILE REFERENCE: L0461/7052
; CURRENT APPLICATION NUMBER: US/09/166,448
; CURRENT FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-166-448-26

Query Match 88.6%; Score 39; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.14; Length 14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VAEVHFL 9
Db 1 VAEVHFL 8
|||||

RESULT 19
US-09-697-884-26
; Sequence 26, Application US/09697884
; Patent No. 6426217
; GENERAL INFORMATION:
; APPLICANT: Chau, Pascal
; APPLICANT: Vantomme, Valrie
; APPLICANT: Stroobant, Vincent
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Thielemans, Kris
; APPLICANT: Corthals, Jurgen
; TITLE OF INVENTION: MAGE-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES
; FILE REFERENCE: L0461/7052
; CURRENT APPLICATION NUMBER: US/09/697,884
; CURRENT FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: 09/166,448
; PRIOR FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26

```
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-697-884-26

Query Match      88.6%; Score 39; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 VAEVHFL 9
Db      1 VAEVHFL 8

RESULT 20
US-09-166-448-25
; Sequence 25, Application US/09166448
; Patent No. 6291430
; GENERAL INFORMATION:
; APPLICANT: Chauv, Pascal
; APPLICANT: Vantomme, Valrie
; APPLICANT: Stroobant, Vincent
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Thielemans, Kris
; APPLICANT: Corthals, Jurgen
; TITLE OF INVENTION: MAGE-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES
; FILE REFERENCE: L0461/7052
; CURRENT APPLICATION NUMBER: US/09/166,448
; CURRENT FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-166-448-25

Query Match      88.6%; Score 39; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 VAEVHFL 9
Db      1 VAEVHFL 8

RESULT 21
US-09-697-884-25
; Sequence 25, Application US/09697884
; Patent No. 6426217
; GENERAL INFORMATION:
; APPLICANT: Chauv, Pascal
; APPLICANT: Vantomme, Valrie
; APPLICANT: Stroobant, Vincent
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Thielemans, Kris
; APPLICANT: Corthals, Jurgen
; TITLE OF INVENTION: MAGE-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES
; FILE REFERENCE: L0461/7052
; CURRENT APPLICATION NUMBER: US/09/697,884
; CURRENT FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: 09/166,448
; PRIOR FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-697-884-25

Query Match      88.6%; Score 39; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 VAEVHFL 9
Db      1 VAEVHFL 8

RESULT 22
US-09-166-448-24
; Sequence 24, Application US/09166448
; Patent No. 6291430
; GENERAL INFORMATION:
; APPLICANT: Chauv, Pascal
; APPLICANT: Vantomme, Valrie
; APPLICANT: Stroobant, Vincent
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Thielemans, Kris
; APPLICANT: Corthals, Jurgen
; TITLE OF INVENTION: MAGE-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES
; FILE REFERENCE: L0461/7052
; CURRENT APPLICATION NUMBER: US/09/166,448
; CURRENT FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-166-448-24

Query Match      88.6%; Score 39; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 VAEVHFL 9
Db      1 VAEVHFL 8

RESULT 23
US-09-697-884-24
; Sequence 24, Application US/09697884
; Patent No. 6426217
; GENERAL INFORMATION:
; APPLICANT: Chauv, Pascal
; APPLICANT: Vantomme, Valrie
; APPLICANT: Stroobant, Vincent
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Thielemans, Kris
; APPLICANT: Corthals, Jurgen
; TITLE OF INVENTION: MAGE-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES
; FILE REFERENCE: L0461/7052
; CURRENT APPLICATION NUMBER: US/09/697,884
; CURRENT FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: 09/166,448
; PRIOR FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-697-884-24

Query Match      88.6%; Score 39; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 VAEVHFL 9
```

```
Db      1  VAEVLVHFL 8
|||||||
RESULT 24
US-08-217-188A-3
; Sequence 3, Application US/08217188A
; Patent No. 5554724
; GENERAL INFORMATION:
; APPLICANT: Melief, Cornelis J. M.
; APPLICANT: Visseren, M. J. W.
; APPLICANT: Kast, W. M.
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated Tumor Rejection Antigen
; TITLE OF INVENTION: Precursor MAGE-2 Derived Peptides, and Uses Thereof
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/217,188A
; FILING DATE: 24-MARCH-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5554724man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5340
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acid residues
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-217-188A-3
Query Match      84.1%; Score 37; DB 1; Length 9;
Best Local Similarity 77.8%; Pred. No. 3e+05;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1  KVAELVHFL 9
|:|||||
Db      1  KMVELVHFL 9
|:|||||

RESULT 25
US-08-687-226-3
; Sequence 3, Application US/08687226
; Patent No. 5686068
; GENERAL INFORMATION:
; APPLICANT: Melief, Cornelis J. M.; Visseren, M. W.;
; APPLICANT: van der Burg, Sjoerd; van der Bruggen, Pierre;
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated Peptides Derived From
; TITLE OF INVENTION: MAGE-2, Cytolytic T Cells Specific To Complexes Of
; TITLE OF INVENTION: Peptides And HLA-A2 Molecules, And Uses Thereof
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City

Qy      1  KVAELVHFL 9
|:|||||
Db      1  KMVELVHFL 9
|:|||||

RESULT 26
US-08-667-725B-3
; Sequence 3, Application US/08667725B
; Patent No. 6063900
; GENERAL INFORMATION:
; APPLICANT: Melief, Cornelis J. M.
; APPLICANT: Visseren, M. J. W.
; APPLICANT: Kast, W. M.
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated Tumor Rejection Antigen
; TITLE OF INVENTION: Precursor MAGE-2 Derived Peptides, and Uses Thereof
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski LLP
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/667,725B
; FILING DATE: 21 June 1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6063900man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5340.1 DIV (081585)
; TELECOMMUNICATION INFORMATION:
```



```

;
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acid residues
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-667-725B-3
Query Match      84.1%; Score 37; DB 3; Length 9;
Best Local Similarity 77.8%; Pred. No. 3e+05;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVAELVHFL 9
   |: |||||
Db 1 KMVELVHFL 9

RESULT 27
US-09-007-748-3
; Sequence 3, Application US/09007748
; Patent No. 6147187
; GENERAL INFORMATION:
; APPLICANT: Melief, Cornelis J. M.
; APPLICANT: Visseren, M. J. W.
; APPLICANT: Kast; W. M.
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated Tumor Rejection Antigen
; TITLE OF INVENTION: Precursor MAGE-2 Derived Peptides, and Uses Thereof
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski LLP
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/007,748
; FILING DATE: 15 January 1998
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6147187man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5340.2 DIV (081572)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acid residues
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-007-748-3
Query Match      84.1%; Score 37; DB 3; Length 9;
Best Local Similarity 77.8%; Pred. No. 3e+05;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVAELVHFL 9
   |: |||||
Db 1 KMVELVHFL 9

RESULT 28
US-09-007-748-3
; Sequence 3, Application US/09183931C
; Patent No. 6210886
; GENERAL INFORMATION:
; APPLICANT: Van Baren, Nicolas
; APPLICANT: Brasseur, Francis
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: METHOD FOR DIAGNOSING LEUKEMIA BY DETERMINING
; TITLE OF INVENTION: TUMOR REJECTION ANTIGEN PRECURSORS
; FILE REFERENCE: LUD 5527.1-JEL/ES
; CURRENT APPLICATION NUMBER: US/09/183,931C
; CURRENT FILING DATE: 2000-02-28
; EARLIER APPLICATION NUMBER: US 09/018,422
; EARLIER FILING DATE: 1998 - 02 - 04
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 31
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION:
US-09-183-931-31
Query Match      84.1%; Score 37; DB 3; Length 9;
Best Local Similarity 77.8%; Pred. No. 3e+05;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVAELVHFL 9
   |: |||||
Db 1 KMVELVHFL 9

RESULT 29
US-09-705-160-31
; Sequence 31, Application US/09705160
; Patent No. 6387630
; GENERAL INFORMATION:
; APPLICANT: Van Baren, Nicolas
; APPLICANT: Brasseur, Francis
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: METHOD FOR DIAGNOSING LEUKEMIA BY DETERMINING
; TITLE OF INVENTION: TUMOR REJECTION ANTIGEN PRECURSORS
; FILE REFERENCE: LUD 5527.3-JEL/MAS
; CURRENT APPLICATION NUMBER: US/09/705,160
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: US 09/183,931
; PRIOR FILING DATE: 1998 - 10 - 30
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 31
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION:
US-09-705-160-31
Query Match      84.1%; Score 37; DB 4; Length 9;
Best Local Similarity 77.8%; Pred. No. 3e+05;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVAELVHFL 9
   |: |||||
Db 1 KMVELVHFL 9

RESULT 30
US-08-197-484-81
; Sequence 81, Application US/08197484
; Patent No. 6419931
; GENERAL INFORMATION:
; APPLICANT: VITIELLO, Maria A.
; APPLICANT: CHESTNUT, Robert W.
; APPLICANT: SETTE, Alessandro D.
```

;; APPLICANT: CELIS, Esteban
;; APPLICANT: GRAY, Howard
;; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
;; TITLE OF INVENTION: CTL IMMUNITY
;; NUMBER OF SEQUENCES: 153
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Townsend and Townsend Kourie and Crew
;; STREET: Steuart Street Tower, One Market Plaza
;; CITY: San Francisco
;; STATE: California
;; COUNTRY: US
;; ZIP: 94105-1493
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/197,484
;; FILING DATE: 16-FEB-1994
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/935,811
;; FILING DATE: 26-AUG-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/874,491
;; FILING DATE: 27-APR-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/827,682
;; FILING DATE: 29-JAN-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 14137-26-4
;; FILING DATE: 26-AUG-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Parmelee, Steven W.
;; REGISTRATION NUMBER: 31,990
;; REFERENCE/DOCKET NUMBER: 14137-26-4
;; TELEPHONE: (206) 467-9600
;; TELEFAX: (206) 623-6793
;; INFORMATION FOR SEQ ID NO: 81:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 9 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: unknown
;; TOPOLOGY: unknown
;; MOLECULE TYPE: peptide
;; US-08-197-484-81

Query Match 84.1%; Score 37; DB 4; Length 9;
Best Local Similarity 77.8%; Pred. No. 3e+05;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVAELVHFL 9
|: |||||
Db 1 KMVELVHFL 9

RESULT 31
US-08-197-484-140
; Sequence 140, Application US/08197484
; Patent No. 6419931
; GENERAL INFORMATION:
; APPLICANT: VITTELLO, Maria A.
; APPLICANT: CHESTNUT, Robert W.
; APPLICANT: SETTE, Alessandro D.
; APPLICANT: CELIS, Esteban
; APPLICANT: GRAY, Howard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
; TITLE OF INVENTION: CTL IMMUNITY
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew

;; STREET: Steuart Street Tower, One Market Plaza
;; CITY: San Francisco
;; STATE: California
;; COUNTRY: US
;; ZIP: 94105-1493
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/197,484
;; FILING DATE: 16-FEB-1994
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/935,811
;; FILING DATE: 26-AUG-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/874,491
;; FILING DATE: 27-APR-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/827,682
;; FILING DATE: 29-JAN-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/749,568
;; FILING DATE: 26-AUG-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Parmelee, Steven W.
;; REGISTRATION NUMBER: 31,990
;; REFERENCE/DOCKET NUMBER: 14137-26-4
;; TELEPHONE: (206) 467-9600
;; TELEFAX: (206) 623-6793
;; INFORMATION FOR SEQ ID NO: 140:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 9 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: unknown
;; TOPOLOGY: unknown
;; MOLECULE TYPE: peptide
;; US-08-197-484-140

Query Match 84.1%; Score 37; DB 4; Length 9;
Best Local Similarity 77.8%; Pred. No. 3e+05;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVAELVHFL 9
|: |||||
Db 1 KMVELVHFL 9

RESULT 32
PCT-US95-02121-81
; Sequence 81, Application PC/TUS9502121
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
; TITLE OF INVENTION: CTL IMMUNITY
; NUMBER OF SEQUENCES: 153
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/02121
; FILING DATE: 16-FEB-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/197,484
; FILING DATE: 16-FEB-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/935,811

;; FILING DATE: 26-AUG-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/874,491
;; FILING DATE: 27-APR-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/827,682
;; FILING DATE: 29-JAN-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/749,568
;; FILING DATE: 26-AUG-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Parmelee, Steven W.
;; REGISTRATION NUMBER: 31,990
;; REFERENCE/DOCKET NUMBER: 14137-26-4PC
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (206) 467-9600
;; TELEFAX: (415) 543-5043
;; INFORMATION FOR SEQ ID NO: 81:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 9 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: unknown
;; TOPOLOGY: unknown
;; MOLECULE TYPE: peptide
PCT-US95-02121-81

Query Match 84.1%; Score 37; DB 5; Length 9;
Best Local Similarity 77.8%; Pred. No. 3e+05;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVAELVHFL 9
|: |||||
Db 1 KMVELVHFL 9

RESULT 33
PCT-US95-02121-140
; Sequence 140, Application PC/TUS9502121
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
; TITLE OF INVENTION: CTL IMMUNITY
; NUMBER OF SEQUENCES: 153
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/02121
; FILING DATE: 16-FEB-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/197,484
; FILING DATE: 16-FEB-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/935,811
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/874,491
; FILING DATE: 27-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,682
; FILING DATE: 29-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/749,568
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 14137-26-4PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600

;; TELEFAX: (415) 543-5043
;; INFORMATION FOR SEQ ID NO: 140:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 9 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: unknown
;; TOPOLOGY: unknown
;; MOLECULE TYPE: peptide
PCT-US95-02121-140

Query Match 84.1%; Score 37; DB 5; Length 9;
Best Local Similarity 77.8%; Pred. No. 3e+05;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVAELVHFL 9
|: |||||
Db 1 KMVELVHFL 9

RESULT 34
US-08-217-188A-20
; Sequence 20, Application US/08217188A
; Patent No. 5554724
; GENERAL INFORMATION:
; APPLICANT: Melief, Cornelis J. M.
; APPLICANT: Visseren, M. J. W.
; APPLICANT: Kast, W. M.
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated Tumor Rejection Antigen
; TITLE OF INVENTION: Precursor MAGE-2 Derived Peptides, and Uses Thereof
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/217,188A
; FILING DATE: 24-MARCH-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5554724man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5340
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acid residues
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-217-188A-20

Query Match 84.1%; Score 37; DB 1; Length 10;
Best Local Similarity 77.8%; Pred. No. 0.24;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVAELVHFL 9
|: |||||
Db 1 KMVELVHFL 9

RESULT 35

US-08-687-226-20
; Sequence 20, Application US/08687226
; Patent No. 5686068
; GENERAL INFORMATION:
; APPLICANT: Melief, Cornelis J. M.; Visseren, M. W.;
; APPLICANT: van der Burg, Sjoerd; van der Bruggen, Pierre;
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated Peptides Derived From
; TITLE OF INVENTION: Mage-2, Cytolytic T Cells Specific To Complexes Of
; TITLE OF INVENTION: Peptides And HLA-A2 Molecules, And Uses Thereof
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/687,226
; FILING DATE: 25-JULY-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/217,188
; FILING DATE: 24-MARCH-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5686068man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5447
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 688-9200
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acid residues
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-687-226-20
Query Match 84.1%; Score 37; DB 1; Length 10;
Best Local Similarity 77.8%; Pred. No. 0.24;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 KVAELVHFL 9
|: |||||
Db 1 KMVELVHFL 9
|: |||||
RESULT 36
US-08-667-725B-20
; Sequence 20, Application US/0866725B
; Patent No. 6063900
; GENERAL INFORMATION:
; APPLICANT: Melief, Cornelis J. M.
; APPLICANT: Visseren, M. J. W.
; APPLICANT: Kast; W. M.
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated Tumor Rejection Antigen
; TITLE OF INVENTION: Precursor Mage-2 Derived Peptides, and Uses Thereof
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski LLP
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10013
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/007,748
; FILING DATE: 15 January 1998
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6147187man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5340.2 DIV (081572)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acid residues

ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/667,725B
; FILING DATE: 21 June 1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6063900man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5340.1 DIV (081585)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acid residues
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-667-725B-20
Query Match 84.1%; Score 37; DB 3; Length 10;
Best Local Similarity 77.8%; Pred. No. 0.24;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 KVAELVHFL 9
|: |||||
Db 1 KMVELVHFL 9
|: |||||
RESULT 37
US-09-007-748-20
; Sequence 20, Application US/09007748
; Patent No. 6147187
; GENERAL INFORMATION:
; APPLICANT: Melief, Cornelis J. M.
; APPLICANT: Visseren, M. J. W.
; APPLICANT: Kast; W. M.
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated Tumor Rejection Antigen
; TITLE OF INVENTION: Precursor Mage-2 Derived Peptides, and Uses Thereof
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski LLP
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/007,748
; FILING DATE: 15 January 1998
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6147187man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5340.2 DIV (081572)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acid residues

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-007-748-20

Query Match 84.1%; Score 37; DB 3; Length 10;
Best Local Similarity 77.8%; Pred. No. 0.24;
Matches 7; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

Qy 1 KVAELVHFL 9
|: |||||
Db 1 KMVELVHFL 9

RESULT 38
US-08-197-484-82
; Sequence 82, Application US/08197484
; Patent No. 6419931
; GENERAL INFORMATION:
; APPLICANT: VITIELLO, Maria A.
; APPLICANT: CHESTNUT, Robert W.
; APPLICANT: SETTE, Alessandro D.
; APPLICANT: CELIS, Esteban
; APPLICANT: GRAY, Howard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
; TITLE OF INVENTION: CTL IMMUNITY
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: Stuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/197,484
; FILING DATE: 16-FEB-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/935,811
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/874,491
; FILING DATE: 27-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,682
; FILING DATE: 29-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/749,568
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 14137-26-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (206) 623-6793
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-197-484-82

Query Match 84.1%; Score 37; DB 4; Length 10;
Best Local Similarity 77.8%; Pred. No. 0.24;

Matches 7; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

Qy 1 KVAELVHFL 9
|: |||||
Db 1 KMVELVHFL 9

RESULT 39
US-08-197-484-141
; Sequence 141, Application US/08197484
; Patent No. 6419931
; GENERAL INFORMATION:
; APPLICANT: VITIELLO, Maria A.
; APPLICANT: CHESTNUT, Robert W.
; APPLICANT: SETTE, Alessandro D.
; APPLICANT: CELIS, Esteban
; APPLICANT: GRAY, Howard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
; TITLE OF INVENTION: CTL IMMUNITY
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: Stuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/197,484
; FILING DATE: 16-FEB-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/935,811
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/874,491
; FILING DATE: 27-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,682
; FILING DATE: 29-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/749,568
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 14137-26-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (206) 623-6793
; INFORMATION FOR SEQ ID NO: 141:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-197-484-141

Query Match 84.1%; Score 37; DB 4; Length 10;
Best Local Similarity 77.8%; Pred. No. 0.24;
Matches 7; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

Qy 1 KVAELVHFL 9
|: |||||
Db 1 KMVELVHFL 9

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RESULT 40
PCT-US95-02121-82
; Sequence 82, Application PC/TUS9502121
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
; TITLE OF INVENTION: CTL IMMUNITY
; NUMBER OF SEQUENCES: 153
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/02121
; FILING DATE: 16-FEB-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/197,484
; FILING DATE: 16-FEB-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/935,811
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/874,491
; FILING DATE: 27-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,682
; FILING DATE: 29-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/749,568
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 14137-26-4PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
PCT-US95-02121-82

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Query Match      84.1%; Score 37; DB 5; Length 10;
Best Local Similarity 77.8%; Pred. No. 0.24;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 KVAELVHFL 9
      | : |||||
Db      1 KMWELVHFL 9

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Search completed: July 23, 2004, 12:53:44
Job time : 19 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 23, 2004, 12:52:52 ; Search time 42 Seconds
(without alignments)
67.104 Million cell updates/sec

Title: US-09-458-298b-711

Perfect score: 44

Sequence: 1 KVAVLVHPL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1288442 seqs, 313154207 residues

Total number of hits satisfying chosen parameters: 1288442

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
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8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
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11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	44	100.0	9	12	US-10-149-135-367
2	44	100.0	9	12	US-10-149-135-711
3	44	100.0	9	12	US-10-149-135-2214
4	44	100.0	9	12	US-10-149-135-2282
5	44	100.0	9	12	US-10-149-135-2357
6	44	100.0	9	12	US-10-149-135-2372
7	44	100.0	9	14	US-10-116-118-4
8	44	100.0	9	14	US-10-116-118-46
9	44	100.0	10	12	US-10-149-135-368
10	44	100.0	10	12	US-10-149-135-712
11	44	100.0	10	12	US-10-149-135-900
12	44	100.0	10	12	US-10-149-135-2283
13	44	100.0	10	12	US-10-149-135-2358
14	44	100.0	10	12	US-10-149-135-2373
15	44	100.0	11	12	US-10-149-135-369

16	44	100.0	11	12	US-10-149-135-713	Sequence 713, App
17	44	100.0	11	12	US-10-149-135-901	Sequence 901, App
18	44	100.0	11	12	US-10-149-135-905	Sequence 905, App
19	44	100.0	15	12	US-10-149-135-2003	Sequence 2003, App
20	44	100.0	16	14	US-10-170-832-3	Sequence 3, Appli
21	44	100.0	30	12	US-10-296-734-1296	Sequence 1296, Ap
22	44	100.0	221	9	US-09-784-199-4	Sequence 4, Appli
23	44	100.0	314	9	US-09-766-889A-55	Sequence 55, Appli
24	44	100.0	314	9	US-09-784-199-2	Sequence 2, Appli
25	44	100.0	314	10	US-09-860-840-2	Sequence 2, Appli
26	44	100.0	314	10	US-09-849-602-29	Sequence 29, Appl
27	44	100.0	314	12	US-10-149-135-2440	Sequence 2440, Ap
28	44	100.0	314	12	US-10-296-734-829	Sequence 829, App
29	44	100.0	314	14	US-10-146-473-53	Sequence 53, Appl
30	44	100.0	314	14	US-10-177-390-20	Sequence 20, Appl
31	44	100.0	314	14	US-10-170-832-2	Sequence 2, Appli
32	44	100.0	314	15	US-10-117-937-73	Sequence 73, Appl
33	44	100.0	314	16	US-10-444-683-2	Sequence 2, Appli
34	44	100.0	315	14	US-10-093-766-40	Sequence 40, Appl
35	44	100.0	315	14	US-10-157-031-54	Sequence 54, Appl
36	44	100.0	315	15	US-10-295-027-366	Sequence 366, App
37	44	100.0	3541	12	US-10-296-770-2	Sequence 2, Appli
38	44	100.0	3541	12	US-10-296-734-1454	Sequence 1454, Ap
39	42	95.5	9	9	US-09-894-018-321	Sequence 321, App
40	42	95.5	9	14	US-10-116-118-5	Sequence 5, Appli
41	42	95.5	144	9	US-09-894-018-129	Sequence 129, App
42	42	95.5	147	9	US-09-894-018-131	Sequence 131, App
43	42	95.5	148	9	US-09-894-018-127	Sequence 127, App
44	41	93.2	9	12	US-10-149-135-2215	Sequence 2215, Ap
45	41	93.2	9	12	US-10-149-135-2216	Sequence 2216, Ap

ALIGNMENTS

RESULT 1

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US-10-149-135-367
; Sequence 367, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fixes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; TITLE OF INVENTION: MAGS2/3 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0130001
; CURRENT APPLICATION NUMBER: US/10/149,135
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 367
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
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OTHER INFORMATION: Artificial Peptide
US-10-149-135-367

Query Match 100.0%; Score 44; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVAELVHFL 9
| | | | | | | | |
Db 1 KVAELVHFL 9

RESULT 2

US-10-149-135-711
Sequence 711, Application US/10149135
Publication No. US20040053822A1
GENERAL INFORMATION:
APPLICANT: Fikes, John
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Celis, Esteban
APPLICANT: Keogh, Elissa

TITLE OF INVENTION: Inducing Cellular Immune Responses to
MAGE2/3 Using Peptide and Nucleic Acid Compositions

FILE REFERENCE: 2060.0130001
CURRENT APPLICATION NUMBER: US/10/149,135
CURRENT FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: PCT/US00/33545
PRIOR FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: US 09/458,298
PRIOR FILING DATE: 1999-12-10
PRIOR APPLICATION NUMBER: US 09/189,702
PRIOR FILING DATE: 1998-11-10
PRIOR APPLICATION NUMBER: US 08/205,713
PRIOR FILING DATE: 1994-03-04
PRIOR APPLICATION NUMBER: US 08/159,184
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/073,205
PRIOR FILING DATE: 1993-06-04
PRIOR APPLICATION NUMBER: US 08/027,146
PRIOR FILING DATE: 1993-03-05
NUMBER OF SEQ ID NOS: 2479
SOFTWARE: PatentIn version 3.1
SEQ ID NO 711
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: Artificial Peptide
US-10-149-135-711

Query Match 100.0%; Score 44; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVAELVHFL 9
| | | | | | | | |
Db 1 KVAELVHFL 9

RESULT 3

US-10-149-135-2214
Sequence 2214, Application US/10149135
Publication No. US20040053822A1
GENERAL INFORMATION:
APPLICANT: Fikes, John
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Celis, Esteban

APPLICANT: Keogh, Elissa
TITLE OF INVENTION: Inducing Cellular Immune Responses to
MAGE2/3 Using Peptide and Nucleic Acid Compositions
FILE REFERENCE: 2060.0130001
CURRENT APPLICATION NUMBER: US/10/149,135
CURRENT FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: PCT/US00/33545
PRIOR FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: US 09/458,298
PRIOR FILING DATE: 1999-12-10
PRIOR APPLICATION NUMBER: US 09/189,702
PRIOR FILING DATE: 1998-11-10
PRIOR APPLICATION NUMBER: US 08/205,713
PRIOR FILING DATE: 1994-03-04
PRIOR APPLICATION NUMBER: US 08/159,184
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/073,205
PRIOR FILING DATE: 1993-06-04
PRIOR APPLICATION NUMBER: US 08/027,146
PRIOR FILING DATE: 1993-03-05
NUMBER OF SEQ ID NOS: 2479
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2214
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Artificial Peptide
US-10-149-135-2214

Query Match 100.0%; Score 44; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVAELVHFL 9
| | | | | | | | |
Db 1 KVAELVHFL 9

RESULT 4

US-10-149-135-2282
Sequence 2282, Application US/10149135
Publication No. US20040053822A1
GENERAL INFORMATION:
APPLICANT: Fikes, John
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Celis, Esteban
APPLICANT: Keogh, Elissa

TITLE OF INVENTION: Inducing Cellular Immune Responses to
MAGE2/3 Using Peptide and Nucleic Acid Compositions

FILE REFERENCE: 2060.0130001
CURRENT APPLICATION NUMBER: US/10/149,135
CURRENT FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: PCT/US00/33545
PRIOR FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: US 09/458,298
PRIOR FILING DATE: 1999-12-10
PRIOR APPLICATION NUMBER: US 09/189,702
PRIOR FILING DATE: 1998-11-10
PRIOR APPLICATION NUMBER: US 08/205,713
PRIOR FILING DATE: 1994-03-04
PRIOR APPLICATION NUMBER: US 08/159,184
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/073,205
PRIOR FILING DATE: 1993-06-04
PRIOR APPLICATION NUMBER: US 08/027,146
PRIOR FILING DATE: 1993-03-05
NUMBER OF SEQ ID NOS: 2479
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2282

; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-2282

Query Match 100.0%; Score 44; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVAELVHFL 9
Db 1 KVAELVHFL 9

RESULT 5

US-10-149-135-2357
; Sequence 2357, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: 2060.0130001
; CURRENT APPLICATION NUMBER: US/10/149,135
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2357
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide

US-10-149-135-2357

US-10-149-135-2357

Query Match 100.0%; Score 44; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVAELVHFL 9
Db 1 KVAELVHFL 9

RESULT 6

US-10-149-135-2372
; Sequence 2372, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro

; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: 2060.0130001
; CURRENT APPLICATION NUMBER: US/10/149,135
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2372
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-2372

Query Match 100.0%; Score 44; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVAELVHFL 9
Db 1 KVAELVHFL 9

RESULT 7

US-10-116-118-4
; Sequence 4, Application US/10116118
; Publication No. US20030143672A1
; GENERAL INFORMATION:
; APPLICANT: Tangri, Shabnam
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioaka, Glenn
; APPLICANT: Fikes, John D.
; TITLE OF INVENTION: Heteroclitic Analogs and Related Methods
; FILE REFERENCE: 2060.0090003
; CURRENT APPLICATION NUMBER: US/10/116,118
; CURRENT FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: US 60/166,529
; PRIOR FILING DATE: 1999-11-18
; PRIOR APPLICATION NUMBER: US 60/239,008
; PRIOR FILING DATE: 2000-10-06
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MAGE3.112
US-10-116-118-4

Query Match 100.0%; Score 44; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY      1 KVAELVHFL 9
      |||||
Db      1 KVAELVHFL 9

RESULT 8
US-10-116-118-46
; Sequence 46, Application US/10116118
; Publication No. US20030143672A1
; GENERAL INFORMATION:
; APPLICANT: Tangri, Shabnam
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn
; APPLICANT: Fikes, John D.
; TITLE OF INVENTION: Heteroclitic Analogs and Related Methods
; FILE REFERENCE: 2060.0090003
; CURRENT APPLICATION NUMBER: US/10/116,118
; PRIOR FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: US 60/166,529
; PRIOR FILING DATE: 1999-11-18
; PRIOR APPLICATION NUMBER: US 60/239,008
; PRIOR FILING DATE: 2000-10-06
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 46
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: MAGE3.122
US-10-116-118-46

Query Match      100.0%; Score 44; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVAELVHFL 9
      |||||
Db      1 KVAELVHFL 9

RESULT 9
US-10-149-135-368
; Sequence 368, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Eteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: 2060.0130001
; CURRENT APPLICATION NUMBER: US/10/149,135
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 712
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-712

Query Match      100.0%; Score 44; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVAELVHFL 9
      |||||
Db      1 KVAELVHFL 9

RESULT 11
US-10-149-135-900
; Sequence 900, Application US/10149135
; Publication No. US20040053822A1
```

GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: 2060.0130001
; CURRENT APPLICATION NUMBER: US/10/149,135
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 900
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-900

Query Match 100.0%; Score 44; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVAELVHFL 9
Db 2 KVAELVHFL 10

RESULT 12
US-10-149-135-2283
; Sequence 2283, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: 2060.0130001
; CURRENT APPLICATION NUMBER: US/10/149,135
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 900
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-900

Query Match 100.0%; Score 44; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVAELVHFL 9
Db 2 KVAELVHFL 10

RESULT 13
US-10-149-135-2358
; Sequence 2358, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: 2060.0130001
; CURRENT APPLICATION NUMBER: US/10/149,135
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2358
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-2358

Query Match 100.0%; Score 44; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVAELVHFL 9
Db 1 KVAELVHFL 9

GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: 2060.0130001
; CURRENT APPLICATION NUMBER: US/10/149,135
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2358
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-2358

Query Match 100.0%; Score 44; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVAELVHFL 9
Db 1 KVAELVHFL 9

RESULT 13
US-10-149-135-2358
; Sequence 2358, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: 2060.0130001
; CURRENT APPLICATION NUMBER: US/10/149,135
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2358
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-2358

Query Match 100.0%; Score 44; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVAELVHFL 9
Db 1 KVAELVHFL 9

```
RESULT 14
US-10-149-135-2373
; Sequence 2373, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: MAGE2/3 Using Peptide and Nucleic Acid Compositions
; CURRENT APPLICATION NUMBER: US/10/149,135
; PRIORITY FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 2373
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-2373
Query Match 100.0%; Score 44; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.049; DB 12; Length 10;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVAELVHFL 9
Db 1 KVAELVHFL 9

RESULT 15
US-10-149-135-369
; Sequence 369, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: MAGE2/3 Using Peptide and Nucleic Acid Compositions
; CURRENT APPLICATION NUMBER: US/10/149,135
; PRIORITY FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
```

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; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 369
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-369
Query Match 100.0%; Score 44; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.054; DB 12; Length 11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVAELVHFL 9
Db 1 KVAELVHFL 9

RESULT 16
US-10-149-135-713
; Sequence 713, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: 2060.0130001
; CURRENT APPLICATION NUMBER: US/10/149,135
; PRIORITY FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 713
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-713
Query Match 100.0%; Score 44; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.054; DB 12; Length 11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVAELVHFL 9
Db 1 KVAELVHFL 9
```

```
Db          1 KVAELVHFL 9
|||||
PRIORITY APPLICATION NUMBER: US 09/458,298
PRIORITY FILING DATE: 1999-12-10
PRIORITY APPLICATION NUMBER: US 09/189,702
PRIORITY FILING DATE: 1998-11-10
PRIORITY APPLICATION NUMBER: US 08/205,713
PRIORITY FILING DATE: 1994-03-04
PRIORITY APPLICATION NUMBER: US 08/159,184
PRIORITY FILING DATE: 1993-11-29
PRIORITY APPLICATION NUMBER: US 08/073,205
PRIORITY FILING DATE: 1993-06-04
PRIORITY APPLICATION NUMBER: US 08/027,146
PRIORITY FILING DATE: 1993-03-05
NUMBER OF SEQ ID NOS: 2479
SOFTWARE: PatentIn version 3.1
SEQ ID NO 905
LENGTH: 11
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Artificial Peptide
US-10-149-135-905

Query Match          100.0%; Score 44; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 KVAELVHFL 9
|||||
Db          3 KVAELVHFL 11
|||||

RESULT 19
US-10-149-135-2003
Sequence 901, Application US/10149135
Publication No. US20040053822A1
GENERAL INFORMATION:
APPLICANT: Fikes, John
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Celis, Eteban
APPLICANT: Keogh, Elissa
TITLE OF INVENTION: Inducing Cellular Immune Responses to
FILE REFERENCE: 2060.0130001
CURRENT APPLICATION NUMBER: US/10/149,135
CURRENT FILING DATE: 2000-12-11
PRIORITY APPLICATION NUMBER: PCT/US00/33545
PRIORITY FILING DATE: 2000-12-11
PRIORITY APPLICATION NUMBER: US 09/458,298
PRIORITY FILING DATE: 1999-12-10
PRIORITY APPLICATION NUMBER: US 09/189,702
PRIORITY FILING DATE: 1998-11-10
PRIORITY APPLICATION NUMBER: US 08/205,713
PRIORITY FILING DATE: 1994-03-04
PRIORITY APPLICATION NUMBER: US 08/159,184
PRIORITY FILING DATE: 1993-11-29
PRIORITY APPLICATION NUMBER: US 08/073,205
PRIORITY FILING DATE: 1993-06-04
PRIORITY APPLICATION NUMBER: US 08/027,146
PRIORITY FILING DATE: 1993-03-05
NUMBER OF SEQ ID NOS: 2479
SOFTWARE: PatentIn version 3.1
SEQ ID NO 901
LENGTH: 11
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Artificial Peptide
US-10-149-135-901

Query Match          100.0%; Score 44; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 KVAELVHFL 9
|||||
Db          2 KVAELVHFL 10
|||||

RESULT 18
US-10-149-135-905
Sequence 905, Application US/10149135
Publication No. US20040053822A1
GENERAL INFORMATION:
APPLICANT: Fikes, John
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Celis, Eteban
APPLICANT: Keogh, Elissa
TITLE OF INVENTION: Inducing Cellular Immune Responses to
FILE REFERENCE: 2060.0130001
CURRENT APPLICATION NUMBER: US/10/149,135
CURRENT FILING DATE: 2000-12-11
PRIORITY APPLICATION NUMBER: PCT/US00/33545
PRIORITY FILING DATE: 2000-12-11
```

Best Local Similarity 100.0%; Pred. No. 0.074; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

Qy 1 KVAELVHFL 9
| | | | |
Db 7 KVAELVHFL 15

RESULT 20

US-10-170-832-3
; Sequence 3, Application US/10170832
; Publication No. US2003017092A1
; GENERAL INFORMATION:
; APPLICANT: Chaux, Pascal
; APPLICANT: Vantomme, Valrie
; APPLICANT: Stroobant, Vincent
; APPLICANT: Boon-falleur, Thierry
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Thielemans, Kris
; APPLICANT: Corthals, Jurgien
; TITLE OF INVENTION: MAG-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES
; FILE REFERENCE: L0461/7052
; CURRENT APPLICATION NUMBER: US/10/170,832
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US/09/166,448
; PRIOR FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-170-832-3

Query Match 100.0%; Score 44; DB 14; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.079; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

Qy 1 KVAELVHFL 9
| | | | |
Db 2 KVAELVHFL 10

RESULT 21

US-10-296-734-1296
; Sequence 1296, Application US/10296734
; Publication No. US20040054137A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Scott A
; APPLICANT: Ramshaw, Ian A
; TITLE OF INVENTION: Synthetic molecules and uses therefor
; FILE REFERENCE: Savine
; CURRENT APPLICATION NUMBER: US/10/296,734
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: AU PQ7761/00
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 1507
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1296
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: MAG-3 segment 8
US-10-296-734-1296

Query Match 100.0%; Score 44; DB 12; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.15; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

Qy 1 KVAELVHFL 9
| | | | |
Db 9 KVAELVHFL 17

RESULT 22

US-09-784-199-4
; Sequence 4, Application US/09784199
; Patent No. US20020164738A1
; GENERAL INFORMATION:
; APPLICANT: MORISHIMA, No. US20020164738A1uhiro
; APPLICANT: SHIBATA, Takehiko
; TITLE OF INVENTION: CELL DEATH INHIBITORY PROTEIN
; FILE REFERENCE: 04853-0057-00000
; CURRENT APPLICATION NUMBER: US/09/784,199
; CURRENT FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: JP 2000-41927
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-784-199-4

Query Match 100.0%; Score 44; DB 9; Length 221;
Best Local Similarity 100.0%; Pred. No. 1.2; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

Qy 1 KVAELVHFL 9
| | | | |
Db 19 KVAELVHFL 27

RESULT 23

US-09-766-889A-55
; Sequence 55, Application US/09766889A
; Patent No. US20020164654A1
; GENERAL INFORMATION:
; APPLICANT: Luiten, Rosalie
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Stroobant, Vincent
; APPLICANT: Demotte, Nathalie
; APPLICANT: Schultz, Erwin
; TITLE OF INVENTION: MAG-3 ANTIGENIC PEPTIDES WHICH BIND HLA-B35 AND HLA-B44
; FILE REFERENCE: L0461/7104
; CURRENT APPLICATION NUMBER: US/09/766,889A
; CURRENT FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/177,242
; PRIOR FILING DATE: 2000-01-20
; PRIOR APPLICATION NUMBER: US 60/243,212
; PRIOR FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 55
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-766-889A-55

Query Match 100.0%; Score 44; DB 9; Length 314;
Best Local Similarity 100.0%; Pred. No. 1.6; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

Qy 1 KVAELVHFL 9
| | | | |
Db 112 KVAELVHFL 120

RESULT 24

US-09-784-199-2
; Sequence 2, Application US/09784199
; Patent No. US20020164738A1
; GENERAL INFORMATION:

```
; APPLICANT: MORISHIMA, No. US20020164738A1uhiro
; APPLICANT: SHIBATA, Takehiko
; TITLE OF INVENTION: CELL DEATH INHIBITORY PROTEIN
; FILE REFERENCE: 04853-0057-00000
; CURRENT APPLICATION NUMBER: US/09/784,199
; CURRENT FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: JP 2000-41927
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-784-199-2

Query Match      100.0%; Score 44; DB 9; Length 314;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVAELVHFL 9
Db      112 KVAELVHFL 120

RESULT 25
US-09-860-840-2
; Sequence 2, Application US/09860840
; Publication No. US20030049723A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Yi
; APPLICANT: Chau, Pascal
; APPLICANT: Boon, Thierry
; APPLICANT: van der Bruggen, Pierre
; TITLE OF INVENTION: WAGE-A3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES
; FILE REFERENCE: L0461/7110 (JRV)
; CURRENT APPLICATION NUMBER: US/09/860,840
; CURRENT FILING DATE: 2001-05-18
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-860-840-2

Query Match      100.0%; Score 44; DB 10; Length 314;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVAELVHFL 9
Db      112 KVAELVHFL 120

RESULT 26
US-09-849-602-29
; Sequence 29, Application US/09849602
; Publication No. US20030165834A1
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew J.
; APPLICANT: Old, Lloyd J.
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Chen, Yao-Tseng
; TITLE OF INVENTION: Colon Cancer Antigen Panel
; FILE REFERENCE: L0461/7105 (JRV)
; CURRENT APPLICATION NUMBER: US/09/849,602
; CURRENT FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 29
; LENGTH: 314
; TYPE: PRT
US-09-849-602-29

Query Match      100.0%; Score 44; DB 9; Length 314;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVAELVHFL 9
Db      112 KVAELVHFL 120

RESULT 27
US-10-149-135-2440
; Sequence 2440, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: 2060.0130001
; CURRENT APPLICATION NUMBER: US/10/149,135
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2440
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-149-135-2440

Query Match      100.0%; Score 44; DB 12; Length 314;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVAELVHFL 9
Db      112 KVAELVHFL 120

RESULT 28
US-10-296-734-829
; Sequence 829, Application US/10296734
; Publication No. US20040054137A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Scott A
; APPLICANT: Ramshaw, Ian A
; TITLE OF INVENTION: Synthetic molecules and uses therefor
; FILE REFERENCE: Savine
; CURRENT APPLICATION NUMBER: US/10/296,734
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: AU PQ7761/00
; PRIOR FILING DATE: 2000-05-26
US-10-296-734-829

Query Match      100.0%; Score 44; DB 12; Length 314;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVAELVHFL 9
Db      112 KVAELVHFL 120
```

```
; NUMBER OF SEQ ID NOS: 1507
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 829
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: MAGE-3 consensus polypeptide
US-10-296-734-829

Query Match      100.0%; Score 44; DB 12; Length 314;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVAELVHFL 9
Db      112 KVAELVHFL 120

RESULT 29
US-10-146-473-53
; Sequence 53, Application US/10146473
; Publication No. US20030108888A1
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew
; APPLICANT: Gout, Ivan
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Gure, Ali
; APPLICANT: Chen, Yao-Tseng
; APPLICANT: Old, Lloyd
; TITLE OF INVENTION: Breast Cancer Antigens
; FILE REFERENCE: L00461/70130(JRV)
; CURRENT APPLICATION NUMBER: US/10/146.473
; CURRENT FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: US 60/291,150
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 53
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-146-473-53

Query Match      100.0%; Score 44; DB 14; Length 314;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVAELVHFL 9
Db      112 KVAELVHFL 120

RESULT 30
US-10-177-390-20
; Sequence 20, Application US/10177390
; Publication No. US20030143743A1
; GENERAL INFORMATION:
; APPLICANT: Schuler, Gerold
; APPLICANT: N.V. Antwerp Innovatiecentrum
; TITLE OF INVENTION: Improved Transfection of Eucaryotic Cells with Linear
; FILE REFERENCE: Polynucleotides by Electroporation
; FILE REFERENCE: 021505wo/JH/ml
; CURRENT APPLICATION NUMBER: US/10/177,390
; CURRENT FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-177-390-20

; NUMBER OF SEQ ID NOS: 1507
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 829
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: MAGE-3 consensus polypeptide
US-10-296-734-829

Query Match      100.0%; Score 44; DB 12; Length 314;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVAELVHFL 9
Db      112 KVAELVHFL 120

RESULT 29
US-10-146-473-53
; Sequence 53, Application US/10146473
; Publication No. US20030108888A1
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew
; APPLICANT: Gout, Ivan
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Gure, Ali
; APPLICANT: Chen, Yao-Tseng
; APPLICANT: Old, Lloyd
; TITLE OF INVENTION: Breast Cancer Antigens
; FILE REFERENCE: L00461/70130(JRV)
; CURRENT APPLICATION NUMBER: US/10/146.473
; CURRENT FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: US 60/291,150
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 53
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-146-473-53

Query Match      100.0%; Score 44; DB 14; Length 314;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVAELVHFL 9
Db      112 KVAELVHFL 120

RESULT 30
US-10-177-390-20
; Sequence 20, Application US/10177390
; Publication No. US20030143743A1
; GENERAL INFORMATION:
; APPLICANT: Schuler, Gerold
; APPLICANT: N.V. Antwerp Innovatiecentrum
; TITLE OF INVENTION: Improved Transfection of Eucaryotic Cells with Linear
; FILE REFERENCE: Polynucleotides by Electroporation
; FILE REFERENCE: 021505wo/JH/ml
; CURRENT APPLICATION NUMBER: US/10/177,390
; CURRENT FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-177-390-20

Query Match      100.0%; Score 44; DB 14; Length 314;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVAELVHFL 9
Db      112 KVAELVHFL 120

RESULT 31
US-10-170-832-2
; Sequence 2, Application US/10170832
; Publication No. US2003017092A1
; GENERAL INFORMATION:
; APPLICANT: Chau, Pascal
; APPLICANT: Vantomme, Valrie
; APPLICANT: Stroobant, Vincent
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Thielemans, Kris
; APPLICANT: Corthals, Jurgen
; TITLE OF INVENTION: MAGE-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES
; FILE REFERENCE: L0461/7052
; CURRENT APPLICATION NUMBER: US/10/170,832
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US/09/166,448
; PRIOR FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-170-832-2

Query Match      100.0%; Score 44; DB 14; Length 314;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVAELVHFL 9
Db      112 KVAELVHFL 120

RESULT 32
US-10-117-937-73
; Sequence 73, Application US/10117937
; Publication No. US20030220239A1
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLLMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 73
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-73

Query Match      100.0%; Score 44; DB 15; Length 314;
```


Best Local Similarity 100.0%; Pred. No. 1.6; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

Qy 1 KVAELVHFL 9
| | | | | | | |
Db 112 KVAELVHFL 120

RESULT 33

US-10-444-683-2
; Sequence 2, Application US/10444683
; Publication No. US20040077045A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Yi
; APPLICANT: Chaux, Pascal
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: van der Bruggen, Pierre
; TITLE OF INVENTION: WAGE PEPTIDES PRESENTED BY HLA CLASS II MOLECULES
; FILE REFERENCE: L00461.70146.US
; CURRENT APPLICATION NUMBER: US/10/444.683
; CURRENT FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 09/860,840
; PRIOR FILING DATE: 2001-05-18
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-444-683-2

Query Match 100.0%; Score 44; DB 16; Length 314;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVAELVHFL 9
| | | | | | | |
Db 112 KVAELVHFL 120

RESULT 34

US-10-093-766-40
; Sequence 40, Application US/10093766
; Publication No. US20030013099A1
; GENERAL INFORMATION:
; APPLICANT: Lasek, Amy W.
; APPLICANT: Jones, David A.
; APPLICANT: Karpf, Adam R.
; TITLE OF INVENTION: GENES REGULATED BY DNA METHYLATION IN COLON TUMORS
; FILE REFERENCE: PA-0047 US
; CURRENT APPLICATION NUMBER: US/10/093.766
; CURRENT FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PERL Program
; SEQ ID NO 40
; LENGTH: 315
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030013099A1 2502336CD1
US-10-093-766-40

Query Match 100.0%; Score 44; DB 14; Length 315;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVAELVHFL 9
| | | | | | | |
Db 111 KVAELVHFL 119

RESULT 35

Remaining Prior Application data removed - See File Wrapper or PALM.

US-10-157-031-54
; Sequence 54, Application US/10157031
; Publication No. US2003010890A1
; GENERAL INFORMATION:
; APPLICANT: Baranova, A. V.
; APPLICANT: Yankovsky, N. K.
; APPLICANT: Kozlov, A. P.
; APPLICANT: Lobashev, A. V.
; APPLICANT: Krukovskaya, L. L.
; TITLE OF INVENTION: In silico screening for phenotype-associated expressed sequences
; FILE REFERENCE: 2760-103
; CURRENT APPLICATION NUMBER: US/10/157.031
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 415
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 54
; LENGTH: 315
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-157-031-54

Query Match 100.0%; Score 44; DB 14; Length 315;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVAELVHFL 9
| | | | | | | |
Db 111 KVAELVHFL 119

RESULT 36

US-10-295-027-366
; Sequence 366, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295.027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1

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; SEQ ID NO 366
; LENGTH: 315
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-366

Query Match      100.0%; Score 44; DB 15; Length 315;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVAELVHFL 9
Db 111 KVAELVHFL 119

RESULT 37
US-10-296-770-2
; Sequence 2, Application US/10296770
; Publication No. US20030104570A1
; GENERAL INFORMATION:
; APPLICANT: Cabezon Silva, Teresa Elisa Virginia
; APPLICANT: Delisse, Anne-Marie Eva Bernande
; TITLE OF INVENTION: Triple Fusion Proteins Comprising
; TITLE OF INVENTION: Ubiquitin Fused Between Thioresoxin and a Polypeptide of
; TITLE OF INVENTION: Interest
; FILE REFERENCE: B45221
; CURRENT APPLICATION NUMBER: US/10/296,770
; CURRENT FILING DATE: 2002-12-13
; PRIOR APPLICATION NUMBER: PCT/EP01/06952
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: GB 0015619.0
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: GB 0026484.6
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 522
; TYPE: PRT
; ORGANISM: Chimaeric (E. coli - human)
US-10-296-770-2

Query Match      100.0%; Score 44; DB 14; Length 522;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVAELVHFL 9
Db 311 KVAELVHFL 319

RESULT 38
US-10-296-734-1454
; Sequence 1454, Application US/10296734
; Publication No. US20040054137A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Scott A
; APPLICANT: Ramshaw, Ian A
; TITLE OF INVENTION: Synthetic molecules and uses therefor
; FILE REFERENCE: Savine
; CURRENT APPLICATION NUMBER: US/10/296,734
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: AU PQ7761/00
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 1507
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1454
; LENGTH: 3541
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Melanoma cancer specific savine
US-10-296-734-1454
```

```
Query Match      100.0%; Score 44; DB 12; Length 3541;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVAELVHFL 9
Db 3400 KVAELVHFL 3408

RESULT 39
US-09-894-018-321
; Sequence 321, Application US/09894018
; Patent No. US20020119127A1
; GENERAL INFORMATION:
; APPLICANT: EPIMUNE, Inc.
; APPLICANT: Sette, Alessandro
; APPLICANT: Chestnut, Robert
; APPLICANT: Livingston, Brian
; APPLICANT: Baker, Denisw
; APPLICANT: Newman, Mark
; APPLICANT: Brown, David
; TITLE OF INVENTION: METHODS AND SYSTEM FOR OPTIMIZING
; TITLE OF INVENTION: MINIGENES AND PEPTIDES THEREBY
; FILE REFERENCE: 39963-20033.00
; CURRENT APPLICATION NUMBER: US/09/894,018
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: PCT/US00/35568
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/173,390
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: US 60/284,221
; PRIOR FILING DATE: 2001-04-16
; NUMBER OF SEQ ID NOS: 368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 321
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Transgenic mouse
US-09-894-018-321

Query Match      95.5%; Score 42; DB 9; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.2e+06;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVAELVHFL 9
Db 1 KVAELVHFL 9

RESULT 40
US-10-116-118-5
; Sequence 5, Application US/10116118
; Publication No. US20030143672A1
; GENERAL INFORMATION:
; APPLICANT: Tangri, Shabnam
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn
; APPLICANT: Fikes, John D.
; TITLE OF INVENTION: Heteroclitic Analogs and Related Methods
; FILE REFERENCE: 2060.0090003
; CURRENT APPLICATION NUMBER: US/10/116,118
; CURRENT FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: US 60/166,529
; PRIOR FILING DATE: 1999-11-18
; PRIOR APPLICATION NUMBER: US 60/239,008
; PRIOR FILING DATE: 2000-10-06
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
US-10-116-118-5
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! FEATURE:
! OTHER INFORMATION: MAGE3.112 I5
US-10-116-118-5

Query Match      95.5%; Score 42; DB 14; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.2e+06;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy      1 KVAELVHFL 9
        ||||:||||
Db      1 KVAEIVHFL 9
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Search completed: July 23, 2004, 12:58:18
Job time : 42 secs

This Page Blank (uspto)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 23, 2004, 12:49:06 ; Search time 16 seconds
(without alignments)
54.108 Million cell updates/sec

Title: US-09-458-298B-711

Perfect score: 44

Sequence: 1 KVAELVHFL 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 78:**

2: PIR2:**

3: PIR3:**

4: PIR4:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	100.0	314	2 JC2361	melanoma antigen M
2	44	100.0	315	2 I38668	melanoma antigen M
3	41	93.2	314	2 I54519	melanoma antigen M
4	40	90.9	133	2 I38663	melanoma antigen M
5	40	90.9	314	2 JC2360	melanoma antigen M
6	40	90.9	968	2 G81743	preprotein translo
7	39	88.6	163	2 D70486	conserved hypothet
8	38	86.4	169	2 H84077	low temperature re
9	37	84.1	314	2 I68899	melanoma antigen M
10	37	84.1	2471	2 T42977	large tegument pro
11	36	81.8	184	2 A82631	hypothetical prote
12	36	81.8	234	2 I38667	melanoma antigen M
13	36	81.8	252	2 D95266	hypothetical prote
14	34	77.3	210	2 A10031	probable two-compo
15	34	77.3	258	2 A95945	probable oxidoredu
16	34	77.3	317	2 I38661	melanoma antigen M
17	34	77.3	461	2 A56239	mannose-6-phosphat
18	34	77.3	524	1 R0KBAP	nif-specific regul
19	34	77.3	2469	2 H36812	hypothetical prote
20	33	75.0	363	2 T19165	hypothetical prote
21	33	75.0	563	2 S49889	probable membrane
22	33	75.0	734	2 T13785	NADH2 dehydrogenas
23	33	75.0	738	2 T14230	NADH2 dehydrogenas
24	33	75.0	738	2 S58612	NADH2 dehydrogenas
25	33	75.0	741	2 T13051	NADH2 dehydrogenas
26	33	75.0	743	2 T12626	NADH2 dehydrogenas
27	33	75.0	743	2 T13073	NADH2 dehydrogenas
28	33	75.0	744	2 T13405	NADH2 dehydrogenas
29	33	75.0	744	2 T13043	NADH2 dehydrogenas

30	33	75.0	804	1 YUMU	sucrose synthase (
31	33	75.0	988	2 T51054	related to alpha-a
32	33	75.0	1557	2 G86419	probable reverse t
33	32	72.7	184	2 T42314	hypothetical prote
34	32	72.7	285	1 D32354	fructose-bisphosph
35	32	72.7	293	2 B90397	membrane conserved
36	32	72.7	357	1 RQECF	DNA replication an
37	32	72.7	357	2 C91208	DNA replication an
38	32	72.7	357	2 E86054	DNA replication an
39	32	72.7	362	2 AF1950	anthranilate phosph
40	32	72.7	376	2 T40591	hypothetical prote
41	32	72.7	421	1 S73416	thymidine phosphor
42	32	72.7	442	2 S73472	probable thiophene
43	32	72.7	501	2 G86460	probable cytochrom
44	32	72.7	507	2 D64083	adenylosuccinate 1
45	32	72.7	511	2 F86460	probable cytochrom

ALIGNMENTS

RESULT 1

JC2361

melanoma antigen MAGE-3 - human

N;Alternate names: MAGE 3 protein

C;Species: Homo sapiens (man)

C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 18-Feb-2000

A;Accession: JC2361; PH1296; I38438

R;Ding, M.; Beck, R.J.; Keller, C.J.; Fenton, R.G.

Biochem. Biophys. Res. Commun. 202, 549-555, 1994

A;Title: Cloning and analysis of MAGE-1-related genes.

A;Reference number: JC2358; MUID:94311935; PMID:8037761

A;Accession: JC2361

A;Molecule type: mRNA

A;Residues: 1-314 <DIN>

A;Experimental source: melanoma cell line DM150

R;Traversari, C.; van der Bruggen, P.; Luescher, I.F.; Lurquin, C.; Chomez, P.; Van Pel,

J. Exp. Med. 176, 1453-1457, 1992

A;Title: A nonapeptide encoded by human gene MAGE-1 is recognized on HLA-A1 by cytolytic

A;Reference number: PH1294; MUID:93018875; PMID:1402688

A;Accession: PH1296

A;Molecule type: DNA

A;Residues: 168-176 <TRA>

R;Gaugler, B.; Van den Eynde, B.; van der Bruggen, P.; Romero, P.; Gaforio, J.J.; De Plaet

J. Exp. Med. 179, 921-930, 1994

A;Title: Human gene MAGE-3 codes for an antigen recognized on a melanoma by autologous cy

A;Reference number: I38438; MUID:94157413; PMID:8113694

A;Accession: I38438

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-314 <RES>

A;Cross-references: EMBL:U03735; NID:9468825; PIDN:AAA17446.1; PID:9468826

C;Genetics:

A;Gene: MAGE-3

C;Superfamily: tumor associated protein MAGE

F;168-176/Region: HLA-A1 binding #status predicted

Query Match 100.0%; Score 44; DB 2; Length 314;

Best Local Similarity 100.0%; Pred. No. 0.22;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVAELVHFL 9

Db 112 KVAELVHFL 120

RESULT 2

I38668

melanoma antigen MAGE-9 - human

C;Species: Homo sapiens (man)

C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 18-Feb-2000

A;Accession: I38668

R;De Plaen, E.; Arden, K.; Traversari, C.; Gaforio, J.J.; Szikora, J.P.; De Smet, C.; Br

oon, T.
Immunogenetics 40, 360-369, 1994
A;Title: Structure, chromosomal localization, and expression of 12 genes of the MAGE fam
A;Reference number: I38659; MUID:95012457; PMID:7927540
A;Accession: I38668
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-315 <RES>
A;Cross-references: EMBL:U10694; NID:G533527; PIDN:AAA68877.1; PID:G533528
C;Genetics:
A;Gene: GDB:MAGEA9; MAGE9
A;Cross-references: GDB:331125
A;Map position: Xp21.3-Xp21.3
A;Introns: #status absent
C;Superfamily: tumor associated protein MAGE

Query Match 100.0%; Score 44; DB 2; Length 315;
Best Local Similarity 100.0%; Pred. No. 0.22; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0

Qy 1 KVAELVHFL 9
|||||
Db 111 KVAELVHFL 119

RESULT 3
I54519
melanoma antigen MAGE-12 - human
N;Alternate names: MAGE 21 protein
C;Species: Homo sapiens (man)
C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 18-Feb-2000
C;Accession: I54519; J23362; PH1295
R;De Plaen, C.; Lurquin, C.; van der Bruggen, P.; De Plaen, E.; Brasseur, F.; Boon, T.
Immunogenetics 39, 121-129, 1994
A;Title: Sequence and expression pattern of the human MAGE2 gene.
A;Reference number: I54519; MUID:94102805; PMID:8276455
A;Accession: I54519
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-314 <DS>
A;Cross-references: GB:I18877; NID:G499345; PIDN:AAA19023.1; PID:G499346
R;Ding, M.; Beck, R.J.; Keller, C.J.; Fenton, R.G.
Biochem. Biophys. Res. Commun. 202, 549-555, 1994
A;Title: Cloning and analysis of MAGE-1-related genes.
A;Reference number: J23358; MUID:94311935; PMID:8037761
A;Accession: J23362
A;Molecule type: mRNA
A;Residues: 1-9,'S',11-186,'D',188-299,'S',301-314 <DIN>
A;Experimental source: melanoma cell line DMI50; MAGE-12f
R;Traversari, C.; van der Bruggen, P.; Luescher, I.F.; Lurquin, C.; Chomez, P.; Van Pel,
J. Exp. Med. 176, 1453-1457, 1992
A;Title: A nonapeptide encoded by human gene MAGE-1 is recognized on HLA-A1 by cytolytic
A;Reference number: PH1294; MUID:93018875; PMID:1402688
A;Accession: PH1295
A;Molecule type: DNA
A;Residues: 168-176 <TRA>
A;Experimental source: MAGE-21
C;Genetics:
A;Gene: GDB:MAGEA12; MAGE12; MAGE-12f
A;Cross-references: GDB:331129
A;Map position: Xq28-Xq28
C;Superfamily: tumor associated protein MAGE
F;168-176/region: HLA-A1 binding #status predicted

Query Match 93.2%; Score 41; DB 2; Length 314;
Best Local Similarity 88.9%; Pred. No. 0.92; Mismatches 1; Indels 0; Gaps 0;
Matches 8; Conservative 1

Qy 1 KVAELVHFL 9
|||||
Db 112 KVAELVHFL 120

RESULT 4
I38663
melanoma antigen MAGE-5 - human (fragments)
C;Species: Homo sapiens (man)
C;Date: 07-Jun-1996 #sequence_revision 18-Feb-2000 #text_change 18-Feb-2000
C;Accession: I38663; I38664; PH1299; PH1300
R;De Plaen, E.; Arden, K.; Traversari, C.; Gaforio, J.J.; Szikora, J.P.; De Smet, C.; Br
oon, T.
Immunogenetics 40, 360-369, 1994
A;Title: Structure, chromosomal localization, and expression of 12 genes of the MAGE fam
A;Reference number: I38659; MUID:95012457; PMID:7927540
A;Accession: I38663
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-124 <DEP1>
A;Cross-references: EMBL:U10689; NID:G533518; PIDN:AAA68873.1; PID:G533519
A;Experimental source: MAGE-5a antigen
A;Accession: I38664
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-124 <DEP2>
A;Cross-references: EMBL:U10690; NID:G533520; PIDN:AAA68874.1; PID:G533521
A;Experimental source: MAGE-5b antigen
A;Note: these sequences seem to be incomplete with respect to other members of the super
R;Traversari, C.; van der Bruggen, P.; Luescher, I.F.; Lurquin, C.; Chomez, P.; Van Pel,
J. Exp. Med. 176, 1453-1457, 1992
A;Title: A nonapeptide encoded by human gene MAGE-1 is recognized on HLA-A1 by cytolytic
A;Reference number: PH1294; MUID:93018875; PMID:1402688
A;Accession: PH1299
A;Molecule type: DNA
A;Residues: 125-133 <TRA1>
A;Experimental source: MAGE 5 protein
A;Accession: PH1300
A;Molecule type: DNA
A;Residues: 125-133 <TRA2>
A;Experimental source: MAGE 51 protein
C;Genetics:
A;Gene: GDB:MAGEA5; MAGE5
A;Cross-references: GDB:331120
A;Map position: Xq28-Xq28
A;Introns: #status absent
C;Superfamily: tumor associated protein MAGE

Query Match 90.9%; Score 40; DB 2; Length 133;
Best Local Similarity 77.8%; Pred. No. 0.62; Mismatches 7; Conservative 2; Indels 0; Gaps 0;
Matches 7

Qy 1 KVAELVHFL 9
|||||
Db 112 KVAELVHFL 120

RESULT 5
J23360
melanoma antigen MAGE-6 - human
N;Alternate names: tumor-associated antigen, MAGE-3b
C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 18-Feb-2000
C;Accession: J23360; PH1301; I38665; G01445
R;Ding, M.; Beck, R.J.; Keller, C.J.; Fenton, R.G.
Biochem. Biophys. Res. Commun. 202, 549-555, 1994
A;Title: Cloning and analysis of MAGE-1-related genes.
A;Reference number: J23358; MUID:94311935; PMID:8037761
A;Accession: J23360
A;Molecule type: mRNA
A;Residues: 1-314 <DIN>
A;Experimental source: melanoma cell line DMI50
R;Traversari, C.; van der Bruggen, P.; Luescher, I.F.; Lurquin, C.; Chomez, P.; Van Pel,
J. Exp. Med. 176, 1453-1457, 1992
A;Title: A nonapeptide encoded by human gene MAGE-1 is recognized on HLA-A1 by cytolytic
A;Reference number: PH1294; MUID:93018875; PMID:1402688
A;Accession: PH1301
A;Molecule type: DNA

A;Residues: 168-176 <TRA>
R;De Plaen, E.; Arden, K.; Traversari, C.; Gaforio, J.J.; Szikora, J.P.; De Smet, C.; B
con, T.
Immunogenetics 40, 360-369, 1994
A;Title: Structure, chromosomal localization, and expression of 12 genes of the MAGE fam
A;Reference number: 138659; MUID:95012457; PMID:7927540
A;Accession: 138665
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-314 <RES>
A;Cross-references: EMBL:U10691; NID:G533522; PIDN:AAAG68875.1; PID:G533523
R;Fenton, R.G.
submitted to the EMBL Data Library, June 1994
A;Reference number: G07126
A;Accession: G01445
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-314 <FEN>
A;Cross-references: EMBL:U10339; NID:G499121; PIDN:AAAL9006.1; PID:G499122
C;Genetics:
A;Gene: GDB:MAGEA6; MAGE6
A;Cross-references: GDB:331121
A;Map position: Xq28-Xq28
A;Introns: #status absent
C;Superfamily: tumor associated protein MAGE
P;168-176/Region: HLA-A1 binding #status predicted

Query Match 90.9%; Score 40; DB 2; Length 314;
Best Local Similarity 88.9%; Pred. No. 1.5;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVAELVHFL 9
|||:|||||
Db 112 KVAELVHFL 120

RESULT 6
G81743
preprotein translocase SecA chain TC0074 [imported] - Chlamydia muridarum (strain Nigg)
C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 17-Nov-2000
C;Accession: G81743
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
A.; C.; Dodson, R.; Gwin, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A;Reference number: A81500; MUID:20150255; PMID:10684935
A;Accession: G81743
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-968 <TET>
A;Cross-references: GB:AR002275; GB:AR002160; NID:G7190108; PIDN:AAF38956.1; PID:G719010
A;Experimental source: strain Nigg (MoPn)
C;Genetics:
A;Gene: TC0074
C;Superfamily: preprotein translocase secA

Query Match 90.9%; Score 40; DB 2; Length 968;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVAELVHF 8
|||||||
Db 255 KVAELVHF 262

RESULT 7
D70486
conserved hypothetical protein aq_2171 - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 23-Dec-2002
C;Accession: D70486
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov

V.
Nature 392, 353-358, 1998
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; MUID:98196666; PMID:9537320
A;Accession: D70486
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-163 <AQF>
A;Cross-references: GB:AE000776; NID:G2984355; PIDN:AAAC07894.1; PID:G2984375; GB:AE000665
A;Experimental source: strain VFS
C;Genetics:
A;Gene: aq_2171
C;Superfamily: phosphatase

Query Match 88.6%; Score 39; DB 2; Length 163;
Best Local Similarity 77.8%; Pred. No. 1.2;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVAELVHFL 9
|||:|||||
Db 152 EVAELIHFL 160

RESULT 8
H84077
low temperature requirement C protein BH3424 [imported] - Bacillus halodurans (strain C-
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C;Accession: H84077
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hirai,
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: H84077
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-169 <STO>
A;Cross-references: GB:AP001518; GB:BA000004; NID:G1017592; PIDN:BAB07143.1; GSPDB:GN001
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH3424

Query Match 86.4%; Score 38; DB 2; Length 169;
Best Local Similarity 87.5%; Pred. No. 2.1;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VAEELVHFL 9
|||:|||||
Db 25 IAEELVHFL 32

RESULT 9
I68889
melanoma antigen MAGE-2 - human
C;Species: Homo sapiens (man)
C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 18-Feb-2000
C;Accession: I68889; PH1294
R;De Smet, C.; Lurquin, C.; van der Bruggen, P.; De Plaen, E.; Brasseur, F.; Boon, T.
Immunogenetics 39, 121-129, 1994
A;Title: Sequence and expression pattern of the human MAGE2 gene.
A;Reference number: I54519; MUID:94102805; PMID:8276455
A;Accession: I68889
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-314 <RES>
A;Cross-references: GB:U11920; NID:G436180; PIDN:AAAL7729.1; PID:G436181
R;Traversari, C.; van der Bruggen, P.; Luescher, I.F.; Lurquin, C.; Chomez, P.; Van Pel,
J. Exp. Med. 176, 1453-1457, 1992
A;Title: A nonapeptide encoded by human gene MAGE-1 is recognized on HLA-A1 by cytolytic
A;Reference number: PH1294; MUID:93018875; PMID:1402688
A;Accession: PH1294
A;Molecule type: DNA
A;Residues: 168-176 <TRA>

C;Genetics:
A;Gene: GDB:MAGEA2; MAGE2
A;Cross-references: GDB:273684
A;Map position: Xq28-Xq28
C;Superfamily: tumor associated protein MAGE

Query Match 84.1%; Score 37; DB 2; Length 314;
Best Local Similarity 77.8%; Pred. No. 6.2;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVAELVHFL 9
|:|||||
Db 112 KMWELVHFL 120

RESULT 10
T42977
large tegument protein - ateline herpesvirus 3 (strain 73)
C;Species: ateline herpesvirus 3
A;Variety: strain 73
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jan-2000
C;Accession: T42977
R;Albrecht, J.C.; Fleckenstein, B.
submitted to the EMBL Data Library, August 1998
A;Description: Primary structure of the herpesvirus ateles genome.
A;Reference number: 222274
A;Accession: T42977
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-2471 <ALB>
A;Cross-references: EMBL:AF083424; PIDN:AAC95588.1
A;Experimental source: strain 73

Query Match 84.1%; Score 37; DB 2; Length 2471;
Best Local Similarity 55.6%; Pred. No. 50;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVAELVHFL 9
|:|||||
Db 1520 KISELIHPI 1528

RESULT 11
A82631
hypothetical protein XF1836 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;Accession: A82631
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequencing
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: A82631
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-184 <STM>
A;Cross-references: GB:AE004005; GB:AE003849; NID:G9106918; PIDN:AAF84642.1; GSPDB:GN001
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H
as-Neto, E.; Docena, C.; El-Dorothy, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A;Reference number: A59328
A;Contents: annotation
A;Gene: MAGE2

C;Genetics:
A;Gene: XF1836
Query Match 81.8%; Score 36; DB 2; Length 184;
Best Local Similarity 87.5%; Pred. No. 5.8;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVAELVHF 8
|:|||||
Db 140 KVGELVHF 147

RESULT 12
I38667
melanoma antigen MAGE-8 - human
C;Species: Homo sapiens (man)
C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 18-Feb-2000
C;Accession: I38667
R;De Plaen, E.; Arden, K.; Traversari, C.; Gaforio, J.J.; Szikora, J.P.; De Smet, C.; Br
oon, T.
Immunogenetics 40, 360-369, 1994
A;Title: Structure, chromosomal localization, and expression of 12 genes of the MAGE fam
A;Reference number: I38659; MUID:95012457; PMID:7927540
A;Accession: I38667
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-234 <RES>
A;Cross-references: EMBL:U10693; NID:G533525; PIDN:AAA68876.1; PID:G533526
C;Genetics:
A;Gene: GDB:MAGEA8; MAGE8
A;Cross-references: GDB:I331123
A;Map position: Xq28-Xq28
A;Introns: #status absent
C;Superfamily: tumor associated protein MAGE

Query Match 81.8%; Score 36; DB 2; Length 234;
Best Local Similarity 88.9%; Pred. No. 7.5;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVAELVHFL 9
|:|||||
Db 115 KVAELVHFL 123

RESULT 13
D95266
hypothetical protein Sma0074 [imported] - Sinorhizobium meliloti (strain 1021) magaplasmi
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C;Accession: D95266
R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows
.; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.;
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti
A;Reference number: A95262; MUID:21396509; PMID:11481432
A;Accession: D95266
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-252 <KUR>
A;Cross-references: GB:AE006469; PIDN:AAK64694.1; PID:G14523094; GSPDB:GN00165
A;Experimental source: strain 1021, megaplasmid pSymA
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, P.; Barloy-Hubler,
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federpiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
neault, P.; Vandenberg, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
A;Contents: annotation
C;Genetics:
A;Gene: Sma0074
A;Genome: plasmid

C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 81.8%; Score 36; DB 2; Length 252;
Best Local Similarity 87.5%; Pred. No. 8;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VAELVHFL 9

Db 226 VADLVHFL 233

RESULT 14

AI0031 Probable two-component response regulator YPO0255 [imported] - Yersinia pestis (strain C

C;Species: Yersinia pestis

C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 15-Sep-2003

C;Accession: AI0031

R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.

deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;

il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,

Nature 413, 523-527, 2001

A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A;Reference number: AB0001; MUID:21470413; PMID:11586360

A;Accession: AI0031

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-210 <KUR>

A;Cross-references: GB:AL590842; PIDN:CAC89116.1; PID:g15978354; GSPDB:GN00175

C;Genetics:

A;Gene: YPO0255

C;Superfamily: response regulator with HTH DNA-binding domain, NarL type; response regul

Query Match 77.3%; Score 34; DB 2; Length 210;

Best Local Similarity 75.0%; Pred. No. 17;

Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVAELVHF 8

Db 195 KVAELIHW 202

RESULT 15

A95945 Probable oxidoreductase, SDR superfamily protein SMB21159 [imported] - Sinorhizobium mel

C;Species: Sinorhizobium meliloti

C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001

C;Accession: A95945

R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmaster, J.; Chain, P.; Vorholter, F.J.; Hernan

Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001

A;Title: The complete sequence of the 1,683-Kb pSymb megaplasmid from the N2-fixing endo

A;Reference number: A95842; MUID:21396508; PMID:11481431

A;Accession: A95945

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-258 <KUR>

A;Cross-references: GB:AL591985; PIDN:CAC49225.1; PID:g15140711; GSPDB:GN00167

A;Experimental source: strain 1021, megaplasmid pSymb

R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,

Pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;

L.; Hyman, R.W.; Jones, T.

Science 293, 668-672, 2001

A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,

hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.

A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.

A;Reference number: A96039; MUID:21368234; PMID:11474104

A;Contents: annotation

C;Genetics:

A;Gene: SMB21159

C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 77.3%; Score 34; DB 2; Length 258;

Best Local Similarity 87.5%; Pred. No. 21;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 VAELVHFL 9

Db 215 VAEAVHFL 222

RESULT 16

I38661 melanoma antigen MAGE-4 - human

N;Alternate names: MAGE 41 protein; melanoma antigen MAGE-X2

C;Species: Homo sapiens (man)

C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 18-Feb-2000

C;Accession: I38661; I38662; PH1297; PH1298; JC2359; G01446

R;De Plaen, E.; Arden, K.; Traversari, C.; Gaforio, J.J.; Szikora, J.P.; De Smet, C.; Bri

con, T.

Immunogenetics 40, 360-369, 1994

A;Title: Structure, chromosomal localization, and expression of 12 genes of the MAGE fam

A;Reference number: I38659; MUID:95012457; PMID:7927540

A;Accession: I38661

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-317 <DEP1>

A;Cross-references: EMBL:U10687; NID:G533514; PIDN:AAA68871.1; PID:G533515

A;Experimental source: antigen MAGE-4a

A;Accession: I38662

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-172, 'T', 174-317 <DEP2>

A;Cross-references: EMBL:U10688; NID:G533516; PIDN:AAA68872.1; PID:G533517

A;Experimental source: antigen MAGE-4b

R;Traversari, C.; van der Bruggen, P.; Luescher, I.F.; Lurquin, C.; Chomez, P.; Van Pel,

J. Exp. Med. 176, 1453-1457, 1992

A;Title: A nonapeptide encoded by human gene MAGE-1 is recognized on HLA-A1 by cytolytic

A;Reference number: PH1294; MUID:93018875; PMID:1402688

A;Accession: PH1297

A;Molecule type: DNA

A;Residues: 169-177 <TRAI>

A;Experimental source: antigen MAGE-4

A;Accession: PH1298

A;Molecule type: DNA

A;Residues: 169-172, 'T', 174-177 <TRA2>

A;Experimental source: antigen MAGE-41

R;Ding, M.; Beck, R.J.; Keller, C.J.; Fenton, R.G.

Biochem. Biophys. Res. Commun. 202, 549-555, 1994

A;Title: Cloning and analysis of MAGE-1-related genes.

A;Reference number: JC2358; MUID:94311935; PMID:8037761

A;Accession: JC2359

A;Molecule type: mRNA

A;Residues: 1-172, 'T', 174-306, 'Q', 308-317 <DIN>

A;Cross-references: EMBL:U10340; NID:g499123; PIDN:AAA19007.1; PID:g499124

A;Experimental source: melanoma cell line DM150

C;Genetics:

A;Gene: GDB:MAGEA4; MAGE4; MAGE-X2

A;Cross-references: GDB:331119

A;Map position: Xq28-Xq28

A;Introns: #status absent

C;Superfamily: tumor associated protein MAGE

P;169-177/Region: HLA-A1 binding #status predicted

Query Match 77.3%; Score 34; DB 2; Length 317;

Best Local Similarity 77.8%; Pred. No. 26;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KVAELVHFL 9

Db 113 KVDELAFHL 121

RESULT 17

A56239

mannose-6-phosphate isomerase (EC 5.3.1.8) - Emericella nidulans

C;Species: Emericella nidulans, Aspergillus nidulans

C;Date: 03-Nov-1995 #sequence_revision 03-Nov-1995 #text_change 24-Sep-1999
 C;Accession: A56239; S31241
 R;Smith, D.J.; Payton, M.A.
 Mol. Cell. Biol. 14, 6030-6038, 1994
 A;Title: Hyphal tip extension in *Aspergillus nidulans* requires the *manA* gene, which encodes a mannosyltransferase.
 A;Reference number: A56239; MUID:94344113; PMID:8065336
 A;Accession: A56239
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-461 <SMI>
 A;Cross-references: GB:M85239; NID:g168071; PIDN:AAA33319.1; PID:g168072
 R;Smith, D.J.; Proudfoot, A.; Friedli, L.; Klüg, L.S.; Paravicini, G.; Payton, M.A.
 Mol. Cell. Biol. 12, 2924-2930, 1992
 A;Title: PMT40, an intron-containing gene required for early steps in yeast mannosylation.
 A;Reference number: S31240; MUID:92318908; PMID:1377774
 A;Accession: S31241
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-461 <SM2>
 A;Cross-references: EMBL:M85239; NID:g168071; PIDN:AAA33319.1; PID:g168072
 C;Superfamily: Yeast mannosyltransferase
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1992
 C;Genetics:
 A;Gene: *manA*
 A;Introns: 11/1; 18/1; 48/3; 128/1
 A;Keywords: intramolecular oxidoreductase; isomerase

Query Match 77.3%; Score 34; DB 2; Length 461;
 Best Local Similarity 75.0%; Pred. No. 38;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VAEIVHFL 9
 :||:||||
 Db 151 LAEIVHFL 158

RESULT 18
 R;Klebsiella pneumoniae
 C;Species: *Klebsiella pneumoniae*
 C;Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 28-Apr-2003
 C;Accession: A91060; A93571; S02513; A03562
 R;Drummond, M.; Whitty, P.; Wootton, J.
 EMBO J. 5, 441-447, 1986
 A;Title: Sequence and domain relationships of *ntnC* and *nifA* from *Klebsiella pneumoniae*.
 A;Reference number: A91060; MUID:86220124; PMID:3011408
 A;Accession: A91060
 A;Status: nucleic acid sequence not shown
 A;Molecule type: DNA
 A;Residues: 1-524 <DRU>
 R;Buikema, W.J.; Szeto, W.W.; Lemley, P.V.; Orme-Johnson, W.H.; Ausubel, F.M.
 Nucleic Acids Res. 13, 4539-4555, 1985
 A;Title: Nitrogen fixation specific regulatory genes of *Klebsiella pneumoniae* and *Rhizobium meliloti*.
 A;Reference number: A93571; MUID:85242120; PMID:2989799
 A;Accession: A93571
 A;Molecule type: DNA
 A;Residues: 1-484 <BUI>
 A;Note: this sequence has only 484 residues due to a frameshift caused by a missing G in the original sequence.
 R;Arnold, W.; Rump, A.; Klipp, W.; Pfeifer, U.B.; Fuehler, A.
 J. Mol. Biol. 203, 715-738, 1988
 A;Title: Nucleotide sequence of a 24,206-base-pair DNA fragment carrying the entire *nifH* gene.
 A;Reference number: S01836; MUID:89094839; PMID:3062178
 A;Accession: S02513
 A;Molecule type: DNA
 A;Residues: 1-524 <ARN>
 A;Cross-references: EMBL:X13303; NID:g43820; PIDN:CAA31682.1; PID:g43838
 C;Comment: This protein, a transcriptional activator, is required for activation of most *nif* genes.
 C;Genetics:
 A;Gene: *nifA*
 C;Superfamily: Response regulator (sigma54-dependent transcriptional activator), FHA tyrosine phosphorylation
 A;Keywords: DNA binding; P-loop; transcription regulation
 F;212-433/Domain: RNA polymerase sigma factor interaction domain homology <SFI>
 F;240-247/Region: nucleotide-binding motif A (P-loop) #status atypical

F;307-311/Region: nucleotide-binding motif B

Query Match 77.3%; Score 34; DB 1; Length 524;
 Best Local Similarity 75.0%; Pred. No. 44;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 VAEIVHFL 9
 :||:||||
 Db 390 IAEIVHFL 397

RESULT 19
 H36812
 hypothetical protein ORF64 - saimiriine herpesvirus 1 (strain 11)
 C;Species: saimiriine herpesvirus 1
 A;Note: host Saimiri sciureus (common squirrel monkey)
 C;Date: 16-Oct-1992 #sequence_revision 16-Oct-1992 #text_change 08-Oct-1999
 C;Accession: H36812
 R;Albrecht, J.
 submitted to the EMBL Data Library, January 1992
 A;Description: Primary structure of the herpesvirus saimiri genome.
 A;Reference number: A36806
 A;Accession: H36812
 A;Molecule type: DNA
 A;Residues: 1-2469 <ALB>
 A;Cross-references: GB:X64346; NID:g60320; PIDN:CAA45687.1; PID:g60385
 R;Albrecht, J.C.; Nicholas, J.; Biller, D.; Cameron, K.R.; Biesinger, B.; Newman, C.; Witte, W.
 J. Virol. 66, 5047-5058, 1992
 A;Title: Primary structure of the herpesvirus saimiri genome.
 A;Reference number: A37309; MUID:92333688; PMID:1321287
 A;Contents: annotation; protein-coding frames
 A;Note: neither protein nor nucleotide sequence is given
 C;Genetics:
 A;Gene: 64

Query Match 77.3%; Score 34; DB 2; Length 2469;
 Best Local Similarity 55.6%; Pred. No. 2.1e+02;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVAELVHFL 9
 :||:||||
 Db 1521 RVTELIHFI 1529

RESULT 20
 T19165
 hypothetical protein C09H10.9 - *Caenorhabditis elegans*
 C;Species: *Caenorhabditis elegans*
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C;Accession: T19165
 R;Ainscough, R.
 submitted to the EMBL Data Library, July 1995
 A;Reference number: Z19082
 A;Accession: T19165
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-363 <WIL>
 A;Cross-references: EMBL:Z50109; PIDN:CAA90440.1; GSPDB:GN00020; CESP:C09H10.9
 A;Experimental source: clone C09H10
 C;Genetics:
 A;Gene: CESP:C09H10.9
 A;Map position: 2
 A;Introns: 30/3; 114/3; 186/2; 232/1; 268/3; 315/1

Query Match 75.0%; Score 33; DB 2; Length 363;
 Best Local Similarity 85.7%; Pred. No. 49;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVAELVH 7
 :||:||||
 Db 62 KIAELVH 68

RESULT 21

S49889
probable membrane protein YIL120w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein YI8277.09
C;Species: Saccharomyces cerevisiae
C;Date: 13-Jan-1995 #sequence_revision 20-Feb-1995 #text_change 19-Apr-2002
C;Accession: S49889
R;Hamlyn, N.; Churcher, C.
submitted to the EMBL Data Library, November 1994
A;Reference number: S49881
A;Accession: S49889
A;Molecule type: DNA
A;Residues: 1-563 <HAM>
A;Cross-references: GB:Z47047; EMBL:Z46833; NID:g603997; PID:g763226; GSPDB:GN00009; MIF

C;Genetics:
A;Gene: SGD:QDR1; MIPS:YIL120W
A;Cross-references: SGD:S0001382
A;Map position: 9L
A;Superfamily: yeast probable membrane protein YIL121W
C;Keywords: transmembrane protein

F;69-85/Domain: transmembrane #status predicted <TM1>
F;109-125/Domain: transmembrane #status predicted <TM2>
F;137-153/Domain: transmembrane #status predicted <TM3>
F;161-177/Domain: transmembrane #status predicted <TM4>
F;197-213/Domain: transmembrane #status predicted <TM5>
F;229-245/Domain: transmembrane #status predicted <TM6>
F;345-361/Domain: transmembrane #status predicted <TM7>
F;424-440/Domain: transmembrane #status predicted <TM8>
F;448-464/Domain: transmembrane #status predicted <TM9>
F;485-501/Domain: transmembrane #status predicted <TM10>
F;513-529/Domain: transmembrane #status predicted <TM11>

Query Match 75.0%; Score 33; DB 2; Length 563;
Best Local Similarity 85.7%; Pred. No. 76;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVAELVH 7
|||
Db 399 KVAELIH 405

RESULT 22

T13785
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Chiococca racemosa chloroplast
C;Species: Chloroplast Chiococca racemosa
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 03-Jun-2002
C;Accession: T13785

R;Bremer, B.
submitted to the EMBL Data Library, November 1998
A;Description: More characters or more taxa for a robust phylogeny: A case study from th
A;Reference number: Z17756
A;Accession: T13785
A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA
A;Residues: 1-734 <BRE>
A;Cross-references: EMBL:AJ130835; PIDN:CAA10211.1
A;Experimental source: specimen voucher: Bremer 2703 (UPS)

C;Genetics:
A;Genome: chloroplast
A;Note: ndhF
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 5
C;Keywords: chloroplast; membrane-associated complex; NAD; oxidoreductase

Query Match 75.0%; Score 33; DB 2; Length 734;
Best Local Similarity 62.5%; Pred. No. 99;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVAELVHF 8
::|
Db 681 RLAEILHF 688

RESULT 23

T14230

NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Ophiorrhiza mungos chloroplast (1
C;Species: Chloroplast Ophiorrhiza mungos
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Jun-2002
C;Accession: T14230

R;Bremer, B.
submitted to the EMBL Data Library, November 1998
A;Description: More characters or more taxa for a robust phylogeny: A case study from the
A;Reference number: Z17756
A;Accession: T14230

A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-738 <BRE>
A;Cross-references: EMBL:AJ130838; PIDN:CAA10214.1
A;Experimental source: specimen voucher: Bremer 3301 (UPS)

C;Genetics:
A;Genome: chloroplast
A;Note: ndhF
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 5
C;Keywords: chloroplast; membrane-associated complex; NAD; oxidoreductase

Query Match 75.0%; Score 33; DB 2; Length 738;
Best Local Similarity 75.0%; Pred. No. 1e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVAELVHF 8
|||
Db 685 KSAELIHF 692

RESULT 24

S58612
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - maize chloroplast
C;Species: Chloroplast Zea mays (maize)
C;Date: 29-Nov-1995 #sequence_revision 19-Jan-1996 #text_change 03-Jun-2002
C;Accession: S58612

R;Maier, R.M.; Neckermann, K.; Igloi, G.L.; Koessel, H.
J. Mol. Biol. 251, 614-628, 1995
A;Title: Complete sequence of the maize chloroplast genome: gene content, hotspots of di
A;Reference number: S58531; MUID:95395841; PMID:7666415
A;Accession: S58612

A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-738 <MAI>
A;Cross-references: EMBL:X86563; NID:g902200; PIDN:CAA60346.1; PID:g902281
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1995

C;Genetics:
A;Genome: chloroplast
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 5
C;Keywords: chloroplast; membrane-associated complex; NAD; oxidoreductase

Query Match 75.0%; Score 33; DB 2; Length 738;
Best Local Similarity 75.0%; Pred. No. 1e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVAELVHF 8
|||
Db 680 KLAELTHF 687

RESULT 25

T13051
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - chrysanthemum chloroplast
C;Species: Chloroplast Dendranthema x grandiflorum (chrysanthemum)
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 03-Jun-2002
C;Accession: T13051

R;Kim, K.J.; Jansen, R.K.
Proc. Natl. Acad. Sci. U.S.A. 92, 10379-10383, 1995
A;Title: NdhF sequence evolution and the major clades in the sunflower family.
A;Reference number: Z17549; MUID:96036088; PMID:7479788
A;Accession: T13051

A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA

A;Residues: 1-741 <KIM>
A;Cross-references: EMBL:L39443; NID:9845317; PID:9845318; PIDN:AAB46929.1
C;Genetics:
A;Genome: chloroplast
A;Note: ndhf
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 5
C;Keywords: chloroplast; membrane-associated complex; NAD; oxidoreductase

Query Match 75.0%; Score 33; DB 2; Length 741;
Best Local Similarity 75.0%; Pred. No. 1e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVAELVHF 8
|:|||||
Db 679 KLAELTHF 686

RESULT 26
T12626
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Achillea millefolium chloroplast
C;Species: chloroplast Achillea millefolium
C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 03-Jun-2002
C;Accession: T12626
R;Kim, K.J.; Jansen, R.K.
Proc. Natl. Acad. Sci. U.S.A. 92, 10379-10383, 1995
A;Title: NdhF sequence evolution and the major clades in the sunflower family.
A;Reference number: Z17549; MUID:96036088; PMID:7479788
A;Accession: T12626
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-743 <KIM>
A;Cross-references: EMBL:L39442; NID:9845185; PID:9845186; PIDN:AAC37440.1
C;Genetics:
A;Genome: chloroplast
A;Note: ndhf
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 5
C;Keywords: chloroplast; membrane-associated complex; NAD; oxidoreductase

Query Match 75.0%; Score 33; DB 2; Length 743;
Best Local Similarity 75.0%; Pred. No. 1e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVAELVHF 8
|:|||||
Db 679 KLAELTHF 686

RESULT 27
T13073
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Eremothamnus marlothianus chloroplast
C;Species: chloroplast Eremothamnus marlothianus
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 03-Jun-2002
C;Accession: T13073
R;Kim, K.J.; Jansen, R.K.
Proc. Natl. Acad. Sci. U.S.A. 92, 10379-10383, 1995
A;Title: NdhF sequence evolution and the major clades in the sunflower family.
A;Reference number: Z17549; MUID:96036088; PMID:7479788
A;Accession: T13073
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-743 <KIM>
A;Cross-references: EMBL:L39424; NID:9845348; PID:9845349; PIDN:AAC37746.1
C;Genetics:
A;Genome: chloroplast
A;Note: ndhf
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 5
C;Keywords: chloroplast; membrane-associated complex; NAD; oxidoreductase

Query Match 75.0%; Score 33; DB 2; Length 743;
Best Local Similarity 75.0%; Pred. No. 1e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVAELVHF 8
|:|||||

Db 679 KLAELAHF 686
|:|||||

RESULT 28
T13485
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Menyanthes trifoliata chloroplast
C;Species: chloroplast Menyanthes trifoliata
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 03-Jun-2002
C;Accession: T13485
R;Kim, K.J.; Jansen, R.K.
Proc. Natl. Acad. Sci. U.S.A. 92, 10379-10383, 1995
A;Title: NdhF sequence evolution and the major clades in the sunflower family.
A;Reference number: Z17549; MUID:96036088; PMID:7479788
A;Accession: T13485
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-744 <KIM>
A;Cross-references: EMBL:L39388; NID:9845605; PID:9845606; PIDN:AAC37458.1
C;Genetics:
A;Genome: chloroplast
A;Note: ndhf
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 5
C;Keywords: chloroplast; membrane-associated complex; NAD; oxidoreductase

Query Match 75.0%; Score 33; DB 2; Length 744;
Best Local Similarity 75.0%; Pred. No. 1e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVAELVHF 8
|:|||||
Db 682 KLAELTHF 689

RESULT 29
T13043
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Dampiera diversifolia chloroplast
C;Species: chloroplast Dampiera diversifolia
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 03-Jun-2002
C;Accession: T13043
R;Kim, K.J.; Jansen, R.K.
Proc. Natl. Acad. Sci. U.S.A. 92, 10379-10383, 1995
A;Title: NdhF sequence evolution and the major clades in the sunflower family.
A;Reference number: Z17549; MUID:96036088; PMID:7479788
A;Accession: T13043
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-744 <KIM>
A;Cross-references: EMBL:L39386; NID:9845321; PID:9845322; PIDN:AAC37742.1
C;Genetics:
A;Genome: chloroplast
A;Note: ndhf
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 5
C;Keywords: chloroplast; membrane-associated complex; NAD; oxidoreductase

Query Match 75.0%; Score 33; DB 2; Length 744;
Best Local Similarity 75.0%; Pred. No. 1e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVAELVHF 8
|:|||||
Db 682 KLAELTHF 689

RESULT 30
YUMU
sucrose synthase (EC 2.4.1.13) - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 11-Jun-1999
C;Accession: S19125
R;Chopra, S.; Del-favero, J.; Dolferus, R.; Jacobs, M.
Plant Mol. Biol. 18, 131-134, 1992
A;Title: Sucrose synthase of Arabidopsis: genomic cloning and sequence characterization.

A;Reference number: S19125; MUID:92119221; PMID:1531031
A;Accession: S19125
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-804 <CHO>
A;Cross-references: EMBL:X60987; NID:g16525; PIDN:CAA43303.1; PID:g16526
C;Genetics:
A;Introns: 31/2; 72/3; 123/2; 187/3; 227/2; 299/3; 331/3; 389/3; 428/3; 484/2; 559/2; 666/2
C;Superfamily: sucrose synthase; sucrose/sucrose-phosphate synthase homology
C;Keywords: Glycosyltransferase; hexosyltransferase
F;276-750/Domain: sucrose/sucrose-phosphate synthase homology <SSPS>

Query Match 75.0%; Score 33; DB 1; Length 804;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVAELVHFL 9
|||:|:|
Db 243 KVSEMVHLL 251

RESULT 31
T51054
related to alpha-adaptin C [imported] - Neurospora crassa
N;Alternate names: protein B12F1.60
C;Species: Neurospora crassa
C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 21-Jul-2000
A;Accession: T51054
R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, R.; Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, R.; submitted to the Protein Sequence Database, July 2000
A;Reference number: 225286
A;Accession: T51054
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-988 <SCH>
A;Cross-references: EMBL:AL390091; GSPDB:GN00116; NCSP:B12F1.60
A;Experimental source: BAC clone B12F1; strain OR74A
C;Genetics:
A;Gene: NCSP:B12F1.60
A;Map position: 6
A;Introns: 70/3; 167/2; 934/3

Query Match 75.0%; Score 33; DB 2; Length 988;
Best Local Similarity 75.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VAEVLVHFL 9
|||:|:|
Db 410 VAEVLVHFL 417

RESULT 32
G86419
Probable reverse transcriptase, 100033-105622 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
A;Accession: G86419
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, J.; Chinn, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Dewar, K.; Huizar, L.; Jensen, N.F.; Hughes, B.; Huizar, L.; Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: G86419
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1557 <STO>
A;Cross-references: GB:AE005172; NID:gl0092236; PIDN:AAG12652.1; GSPDB:GN00141

C;Genetics:
A;Map position: 1

Query Match 75.0%; Score 33; DB 2; Length 1557;
Best Local Similarity 75.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVAELVHFL 8
|||:|:|
Db 1494 KVSELTHP 1501

RESULT 33
T42314
hypothetical protein - phage SPP1
C;Species: phage SPP1
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 11-May-2000
C;Accession: T42314
R;Alonso, J.C.; Luder, G.; Stiege, A.C.; Chai, S.; Weise, F.; Trautner, T.A.
Gene 204, 201-212, 1997
A;Title: The complete nucleotide sequence and functional organization of Bacillus subtilis
A;Reference number: Z22137; MUID:98094274; PMID:9434185
A;Accession: T42314
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-184 <ALO>
A;Cross-references: EMBL:X97918; PIDN:CAA66521.1

Query Match 72.7%; Score 32; DB 2; Length 184;
Best Local Similarity 85.7%; Pred. No. 40;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VAEVLVHFL 8
|||:|:|
Db 62 VAEVLVHFL 68

RESULT 34
D32354
fructose-bisphosphate aldolase (EC 4.1.2.13) fbaA - Bacillus subtilis
N;Alternate names: 30K phosphoprotein orfy-tsrf; fructose-1,6-bisphosphate aldolase
C;Species: Bacillus subtilis
C;Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 16-Jun-2000
C;Accession: S55426; D32354; E32354; D41835; B9621
R;Glaser, P.; Danchin, A.
submitted to the EMBL Data Library, May 1995
A;Description: Cloning and sequencing of the Bacillus subtilis chromosomal region from 3;
A;Reference number: S55414
A;Accession: S55426
A;Molecule type: DNA
A;Residues: 1-285 <GLA>
A;Cross-references: EMBL:Z49782; NID:9853752; PIDN:CAA89873.1; PID:9853765
R;Trach, K.; Chapman, J.W.; Piggot, P.; LeCoq, D.; Hoch, J.A.
J. Bacteriol. 170, 4194-4208, 1988
A;Title: Complete sequence and transcriptional analysis of the spo0F region of the Bacil
A;Reference number: A91883; MUID:98314920; PMID:2457578
A;Accession: D32354
A;Molecule type: DNA
A;Residues: 'MLGWKAFRRQSGYIRTFD', 1-16, 'RVRCRTI' <TR1>
A;Cross-references: GB:M22039
A;Note: this sequence has been revised
A;Note: prior to the correction of a frameshift error, this portion of the sequence was
A;Accession: E32354
A;Molecule type: DNA
A;Residues: 'M', 77-285 <TR2>
A;Cross-references: GB:M22039
A;Note: this sequence has been revised
A;Note: prior to the correction of a frameshift error, this portion of the sequence was
R;Mitchell, C.; Morris, P.W.; Vary, J.C.
J. Bacteriol. 174, 2474-2477, 1992
A;Title: Identification of proteins phosphorylated by ATP during sporulation of Bacillus
A;Reference number: A41835; MUID:92210489; PMID:1556067
A;Accession: D41835

Qy 1 KVAELVHFL 9
| | | | | :
Db 104 KVAELAHLM 112

RESULT 38
E86054
DNA replication and repair protein recF [similarity] - Escherichia coli (strain O157:H7,
C:Species: Escherichia coli
C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 02-Nov-2001
C:Accession: E86054
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimailanta, E.; Potamouisis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: E86054
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-357 <STO>
A:Cross-references: GB:AE005174; MID:gl2518539; PIDN:AGS8897.1; GSPDB:GN00145; UWGP:Z51
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: recF
C:Superfamily: recF protein

Query Match 72.7%; Score 32; DB 2; Length 357;
Best Local Similarity 66.7%; Pred. No. 77;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KVAELVHFL 9
| | | | | :
Db 104 KVAELAHLM 112

RESULT 39
AF1950
anthranilate phosphoribosyltransferase [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C:Accession: AF1950
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AF1950
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-362 <KUR>
A:Cross-references: GB:BA000019; PIDN:BA873110.1; PID:gl7130499; GSPDB:GN00179
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: trpD
C:Superfamily: anthranilate phosphoribosyltransferase; trpD homology

Query Match 72.7%; Score 32; DB 2; Length 362;
Best Local Similarity 66.7%; Pred. No. 78;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVAELVHFL 9
| | | | | :
Db 352 KLAQLVYFL 360

RESULT 40
T40591
hypothetical protein SPBC646.15c - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 04-Mar-2000
C:Accession: T40591
R:Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.

submitted to the EMBL Data Library, January 1999
A:Reference number: Z21938
A:Accession: T40591
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-376 <SEE>
A:Cross-references: EMBL:AL035216; PIDN:CAA22819.1; GSPDB:GN00067; SPDB:SPBC646.15c
A:Experimental source: strain 972h-; cosmid c646
C:Genetics:
A:Gene: SPDB:SPBC646.15c
A:Map position: 2
A:Introns: 49/1; 126/2; 312/2; 350/1
C:Superfamily: Schizosaccharomyces pombe hypothetical protein SPBC646.15c

Query Match 72.7%; Score 32; DB 2; Length 376;
Best Local Similarity 66.7%; Pred. No. 81;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVAELVHFL 9
| | | | | :
Db 99 KVSELYFL 107

Search completed: July 23, 2004, 12:53:15
Job time : 17 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 23, 2004, 12:42:26 ; Search time 14 Seconds
(without alignments)
33.474 Million cell updates/sec

Title: US-09-458-298b-711

Perfect score: 44

Sequence: 1 KVAELVHFL 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	100.0	314	1	MAG3 HUMAN
2	44	100.0	315	1	MAG9 HUMAN
3	41	93.2	314	1	MAGC HUMAN
4	40	90.9	124	1	MAG5 HUMAN
5	40	90.9	314	1	MAG6 HUMAN
6	40	90.9	968	1	SECA CHLMU
7	37	84.1	314	1	MAG2 HUMAN
8	36	81.8	234	1	MAG8 HUMAN
9	36	81.8	373	1	MGE1 HUMAN
10	34	77.3	317	1	MAG4 HUMAN
11	34	77.3	461	1	MANA EMENI
12	34	77.3	524	1	NIFA KLEBOX
13	34	77.3	524	1	NIFA KLEBOX
14	34	77.3	2469	1	TEGU HSUSA
15	33	75.0	563	1	YIMO YEAST
16	33	75.0	738	1	NUSC MAIZE
17	33	75.0	744	1	NUSC DAMDI
18	33	75.0	805	1	SUS2 ARATH
19	32	72.7	285	1	ALF1 BACSU
20	32	72.7	356	1	RECFC ECOLI
21	32	72.7	362	1	TRD2 ANASP
22	32	72.7	421	1	TYPH MYCPN
23	32	72.7	442	1	TRME MYCPN
24	32	72.7	456	1	PUR8 HAEIN
25	32	72.7	527	1	REF1 CANAL
26	32	72.7	710	1	IRAL MOUSE
27	32	72.7	712	1	IRAL HUMAN
28	32	72.7	822	1	EPF8 HUMAN
29	31	70.5	163	1	COAD STRPY
30	31	70.5	230	1	PHOU CAUCR
31	31	70.5	308	1	MGF1 HUMAN
32	31	70.5	309	1	MAG1 HUMAN
33	31	70.5	359	1	RECFL SAUTI
					Q8z2n4 salmonella

ALIGNMENTS

RESULT 1

MAG3 HUMAN	31	70.5	356	1	RECFC SALTY
AC P43357;	31	70.5	401	1	O88A_DROME
DT 01-NOV-1995 (Rel. 32, Created)	31	70.5	610	1	CC20 YEAST
DT 10-OCT-2003 (Rel. 42, Last annotation update)	31	70.5	769	1	RRP3 THOGV
DE Melanoma-associated antigen 3 (MAGB-3 antigen) (Antigen M2Z-D).	31	70.5	880	1	GYRA HAEIN
GN MAGB3 OR MAGB3.	31	70.5	910	1	YO68 CAEEL
OS Homo sapiens (Human).	31	70.5	969	1	SECA_CHLTR
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	31	70.5	5560	1	SPEN_DROME
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	30	68.2	161	1	COAD_STRMU
OX NCBI_TaxID=9606;	30	68.2	166	1	COAD_STRMU
RN [1]	30	68.2	184	1	YCF4_ARATH
RP SEQUENCE FROM N.A., AND MUTAGENESIS.	30	68.2	184	1	YCF4_CARCL
RC TISSUE=Blood;					
RX MEDLINE=94157413; PubMed=8113684;					
RA Gaugier B., van den Eynde B., van der Bruggen P., Romero P.,					
RA Gaforio J.J., de Plaen E., Lethe B., Brasseur F., Boon T.;					
RT "Human gene MAGB-3 codes for an antigen recognized on a melanoma by					
RT autologous cytolytic T lymphocytes.";					
RL J. Exp. Med. 179:921-930(1994).					
RN [2]					
RP SEQUENCE FROM N.A.					
RC TISSUE=Skin;					
RX MEDLINE=94311935; PubMed=8037761;					
RA Ding M., Beck R.J., Keller C.J., Fenton R.G.;					
RT "Cloning and analysis of MAGB-1-related genes.";					
RL Biochem. Biophys. Res. Commun. 202:549-555(1994).					
RN [3]					
RP SEQUENCE FROM N.A.					
RX MEDLINE=20314869; PubMed=10854409;					
RA Mallon A.M., Platzer M., Bates R., Gloeckner G., Botcherby M.,					
RA Nordstiek G., Strivens M.A., Kioschis P., Dangel A., Cunningham D.,					
RA Straw R., Weston P., Hunter C., Gilbert M., Fernando S., Goodall K.,					
RA Kerry G., Gresty J.S., Clark D., Goerdes M., Blechschmidt K.,					
RA Rump A., Hinzmann B., Mundy C.R., Miller W., Poustka A., Herman G.E.,					
RA Rhodes M., Denay P., Rosenthal A., Brown S.D.M.;					
RT "Comparative genome sequence analysis of the Bpa/Str region in mouse					
RT and man.";					
RL Genome Res. 10:758-775(2000).					
RN [4]					
RP SEQUENCE FROM N.A.					
RC TISSUE=Bone marrow, Lung, Prostate, and Skin;					
RX MEDLINE=22398257; PubMed=12477932;					
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,					
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,					
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,					
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,					
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,					
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,					
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,					
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,					
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,					
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,					
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,					

P24900 salmonella
Q9vfn2 drosophila
P26309 saccharomyc
Q9yna4 thogoto vir
P43700 haemophilus
P43607 caenorhabdi
O84707 chlamydia t
Q88x83 drosophila
Q8vnh2 streptococc
P56788 arabidopsis
Q9gdv1 carpobrotus

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RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield V.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Not known, though may play a role in embryonal
CC development and tumor transformation or aspects of tumor
CC progression. Antigen recognized on a melanoma by autologous
CC cytolytic T lymphocytes.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN MANY TUMORS OF SEVERAL TYPES,
CC SUCH AS MELANOMA, HEAD AND NECK SQUAMOUS CELL CARCINOMA, LUNG
CC CARCINOMA AND BREAST CARCINOMA, BUT NOT IN NORMAL TISSUES EXCEPT
CC FOR TESTES AND PLACENTA. NEVER EXPRESSED IN KIDNEY TUMORS,
CC LEUKEMIAS AND LYMPHOMAS.
CC -!- SIMILARITY: Contains 1 MAGE domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U03735; AA017446.1; -
CC EMBL; U02871; -; NOT ANNOTATED_CDS.
CC EMBL; BC000340; AA000340.1; -
CC EMBL; BC005963; AA005963.1; -
CC EMBL; BC011744; AA011744.1; -
CC EMBL; BC016803; AA016803.1; -
CC EMBL; BC017389; AA017389.1; -
CC PIR; JC2361; JC2361.
CC Genew; HGNC:6801; MAGEA3.
CC MIM; 300174; -
CC InterPro; IPR002190; MAGE.
CC Pfam; PF01454; MAGE; 1.
CC PROSITE; PS50838; MAGE; 1.
CC Antigen; Multigene family; Tumor antigen.
CC DOMAIN 109 308
CC MAGE.
CC FT MUTAGEN 170 170 D->A: ABOLISHES HLA-A1 BINDING.
CC FT MUTAGEN 176 176 Y->A: ABOLISHES HLA-A1 BINDING.
CC SEQUENCE 314 AA; 34747 MW; 3F5EB13D1C9946A1 CRC64;
CC -----
CC Query Match 100.0%; Score 44; DB 1; Length 314;
CC Best Local Similarity 100.0%; Pred. No. 0.09;
CC Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC -----
QY 1 KVAELVHFL 9
DB 112 KVAELVHFL 120
RESULT 2
MAG9 HUMAN
ID MAG9 HUMAN STANDARD; PRT; 315 AA.
AC P43362; Q92910;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Melanoma-associated antigen 9 (MAGE-9 antigen).
GN MAGEA9 OR MAGE9.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95012457; PubMed=7927540;
```

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RA de Plaen E., Arden K., Traversari C., Gaforio J.J., Szikora J.-P.,
RA Smet C., Brasseur F., van der Bruggen P., Lethe B., Turquin C.,
RA Blakesley R.W., Chomez P., de Backer O., Cavenee W., Boon T.;
RT "Structure, chromosomal localization, and expression of 12 genes of
RT the MAGE family."
RL Immunogenetics 40:360-369(1994).
RN [2]
RP SEQUENCE FROM N.A.
RA Timms K.M., Bondeson M.L., Ansari-Lari M.A., Lagerstedt K.,
RA Nelson D.L., Pettersson U., Gibbs R.A.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22338257; PubMed=12477932;
RA Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Munzy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield V.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: NOT KNOWN. THOUGH MAY PLAY A ROLE IN EMBRYONAL
CC DEVELOPMENT AND TUMOR TRANSFORMATION OR ASPECTS OF TUMOR
CC PROGRESSION.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN MANY TUMORS OF SEVERAL TYPES,
CC SUCH AS MELANOMA, HEAD AND NECK SQUAMOUS CELL CARCINOMA, LUNG
CC CARCINOMA AND BREAST CARCINOMA, BUT NOT IN NORMAL TISSUES EXCEPT
CC FOR TESTES AND PLACENTA.
CC -!- SIMILARITY: Contains 1 MAGE domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U10694; AAA68877.1; -
CC EMBL; U66083; AAB67888.1; -
CC EMBL; BC002351; AA02351.1; -
CC PIR; I38668; I38668.
CC Genew; HGNC:6807; MAGEA9.
CC MIM; 300342; -
CC InterPro; IPR002190; MAGE.
CC Pfam; PF01454; MAGE; 1.
CC PROSITE; PS50838; MAGE; 1.
CC Antigen; Multigene family; Tumor antigen.
CC DOMAIN 108 307
CC MAGE.
CC FT DOMAIN 34 37
CC FT DOMAIN 87 90 POLY-GLU.
CC SEQUENCE 315 AA; 35088 MW; 7FD2ED10D680D928 CRC64;
CC -----
CC Query Match 100.0%; Score 44; DB 1; Length 315;
CC Best Local Similarity 100.0%; Pred. No. 0.09;
CC Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC -----
QY 1 KVAELVHFL 9
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DR EMBL; U10690; AAA68874.1; -.
DR EMBL; U10689; AAA68873.1; -.
DR PIR; I38663; I38663.
DR Genew; HGNC:6803; MAGEA5.
DR MIM; 300340; -.
DR InterPro; IPR002190; MAGE.
DR Pfam; PF01454; MAGE; 1.
DR PROSITE; PS50838; MAGE; FALSE_NEG.
KW Antigen; Multigene family.
FT DOMAIN 40 43 POLY-SER.
SQ SEQUENCE 124 AA; 13015 MW; 3D8457AFBFD7531E CRC64;

Query Match 90.9%; Score 40; DB 1; Length 124;
Best Local Similarity 77.8%; Pred. No. 0.25;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVAELVHFL 9
Db 112 KVADLIHFL 120

RESULT 5
MAGE6_HUMAN
ID MAGE6_HUMAN STANDARD; PRT; 314 AA.
AC P43360;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Melanoma-associated antigen 6 (MAGE-6 antigen) (MAGE3B).
GN MAGEA6 OR MAGE6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95012457; PubMed=7927540;
RA de Plaen E., Arden K., Traversari C., Gaforio J.J., Szikora J.-P.,
RA de Smet C., Brasseur F., van der Bruggen P., Lethe B., Lurquin C.,
RA Brasseur R., Chomez P., de Backer O., Cavenne W., Boon T.;
RT "Structure, chromosomal localization, and expression of 12 genes of
RT the MAGE family.";
RL Immunogenetics 40:360-369(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Skin;
RX MEDLINE=94311935; PubMed=8037761;
RA Ding M., Beck R.J., Keller C.J., Fenton R.G.;
RT "Cloning and analysis of MAGE-1-related genes.";
RL Biochem. Biophys. Res. Commun. 202:549-555(1994).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=95369706; PubMed=7642112;
RA Imai Y., Shichijo S., Yamada A., Katayama T., Yano H., Itoh K.;
RT "Sequence analysis of the MAGE gene family encoding human tumor-
RT rejection antigens.";
RL Gene 160:287-290(1995).
RN [4]
RP SEQUENCE FROM N.A.
RX TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
RA Raba S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Heiton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,

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RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: NOT KNOWN, THOUGH MAY PLAY A ROLE IN TUMOR
CC OR ASPECTS OF TUMOR PROGRESSION.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN MANY TUMORS OF SEVERAL TYPES,
CC SUCH AS MELANOMA, HEAD AND NECK SQUAMOUS CELL CARCINOMA, LUNG,
CC CARCINOMA AND BREAST CARCINOMA, BUT NOT IN NORMAL TISSUES EXCEPT
CC FOR TESTES.
CC -!- SIMILARITY: Contains 1 MAGE domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U10691; AAA68875.1; -.
DR EMBL; U10339; AAA19006.1; -.
DR EMBL; D32076; BAA06842.1; -.
DR EMBL; BC041599; AAH41599.1; -.
DR PIR; JC2360; JC2360.
DR Genew; HGNC:6804; MAGEA6.
DR MIM; 300176; -.
DR InterPro; IPR002190; MAGE.
DR Pfam; PF01454; MAGE; 1.
DR PROSITE; PS50838; MAGE; 1.
KW Antigen; Multigene family; Tumor antigen.
FT DOMAIN 109 308 MAGE.
FT DOMAIN 40 43 POLY-SER.
SQ SEQUENCE 314 AA; 34891 MW; 29B83C7FAGE50263 CRC64;

Query Match 90.9%; Score 40; DB 1; Length 314;
Best Local Similarity 88.9%; Pred. No. 0.63;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVAELVHFL 9
Db 112 KVAKLVHFL 120

RESULT 6
SECA_CHLMU
ID SECA_CHLMU STANDARD; PRT; 968 AA.
AC Q9PLM5;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Preprotein translocase secA subunit.
GN SECA OR TC0074.
OS Chlamydia muridarum.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=83560;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=MOPn / Nig9;
RX MEDLINE=20150255; PubMed=10684935;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.P., Bass S.,
RA White O., Hickey E.K., Peterson J., Uterback T., Berry K., Danson R.,
RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Salzborg S.L.,
RA Winn M., Nelson W., deBoy R., Kolonay J., McClarty G., Salzborg S.L.,
RA Eisen J., Fraser C.M.;
RT "Genome sequences of Chlamydia trachomatis MOPn and Chlamydia
RT pneumoniae AR39.";
RL Nucleic Acids Res. 28:1397-1406(2000).
CC -!- FUNCTION: Involved in protein export. Interacts with the secY/secE

```

subunits. SecA has a central role in coupling the hydrolysis of ATP to the transfer of pre-secretory periplasmic and outer membrane proteins across the membrane (By similarity).

-!- SUBUNIT: Part of the prokaryotic protein translocation apparatus which comprise secA, secB, secD, secE, secF, secG and secY (By similarity).

-!- SUBCELLULAR LOCATION: Cytoplasmic side of plasma membrane (By similarity).

-!- SIMILARITY: Belongs to the secA family.

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EMBL; AE002275; AAF38956.1; -;
 PIR; G81743; G81743.
 TIGR; TC0074; -;
 InterPro; IPR001650; Helicase_C.
 InterPro; IPR00185; SecA.
 Pfam; PF00271; Helicase_C; 1.
 Pfam; PF01043; SecA protein; 1.
 PRINTS; PR00906; SEC.A.
 TIGRFAMs; TIGR00963; secA; 1.
 PROSITE; PS01312; ATP; 1.
 Protein transport; Membrane; Translocation; Transport;
 Complete proteome.
 NP_BIND 114 121 ATP (POTENTIAL).
 SEQUENCE 968 AA; 110512 MW; 187B5536F547D3FC CRC64;
 Query Match 90.9%; Score 40; DB 1; Length 968;
 Best Local Similarity 100.0%; Pred. No. 1.9;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVAELVHP 8
 Db 255 KVAELVHP 262
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 |||||

RESULT 7
 MAG2_HUMAN
 ID MAG2_HUMAN STANDARD; PRT; 314 AA.
 AC P43356;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Melanoma-associated antigen 2 (MAGE-2 antigen).
 GN (MAGEA2A OR MAGEA2 OR MAGE2) AND (MAGEA2B OR MAGEA2 OR MAGE2).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 (1)
 SEQUENCE FROM N.A.
 RP MEDLINE=94102805; PubMed=8276455;
 RA de Smet C., Lurquin C., van der Bruggen P., de Plaen E., Brasseur F.,
 Boon T.;
 RT "Sequence and expression pattern of the human MAGE2 gene.";
 RL Immunogenetics 39:121-129(1994).
 (2)
 SEQUENCE FROM N.A.
 RP MEDLINE=20314869; PubMed=10854409;
 RA Mallon A.M., Platzer M., Bates R., Gloeckner G., Botcherby M.,
 Nordsiek G., Strivens M.A., Kioschis P., Dangel A., Cunningham D.,
 Straw R., Weston P., Hunter C., Gilbert M., Fernando S., Goodall K.,
 Kerry G., Greystrom J.S., Clark D., Goerdes M., Blechschmidt K.,
 Rump A., Hinzmann B., Mundy C.R., Miller W., Poustka A., Herman G.E.,
 Rhodes M., Denny P., Rosenthal A., Brown S.D.M.;
 RT "Comparative genome sequence analysis of the Bpa/Str region in mouse
 and man.";

Genome Res. 10:758-775(2000).
 (3)
 MUTAGENESIS.
 CC TISSUE=Blood;
 RX MEDLINE=94157413; PubMed=8113684;
 RA Gaugier B., van den Eynde B., van der Bruggen P., Romero P.,
 de Plaen E., Lethe B., Brasseur F., Boon T.;
 RT "Human gene MAGE-3 codes for an antigen recognized on a melanoma by
 autologous cytolytic T lymphocytes.";
 RL J. Exp. Med. 179:921-930(1994).
 CC -!- FUNCTION: Not known, though may play a role in embryonal
 development and tumor transformation or aspects of tumor
 progression. Antigen recognized on a melanoma by autologous
 cytolytic T lymphocytes.
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN MANY TUMORS OF SEVERAL TYPES,
 SUCH AS MELANOMA, HEAD AND NECK SQUAMOUS CELL CARCINOMA, LUNG
 CARCINOMA AND BREAST CARCINOMA, BUT NOT IN NORMAL TISSUES EXCEPT
 FOR TESTES.
 CC -!- SIMILARITY: Contains 1 MAGE domain.
 CC -----
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 or send an email to license@isb-sib.ch).

EMBL; L18920; AAA17729.1; -;
 EMBL; U82671; -; NOT_ANNOTATED_CDS.
 PIR; I68889; I68889.
 Genew; HGNC:6800; MAGEA2.
 MIM; 300173; -;
 InterPro; IPR002190; MAGE.
 Pfam; PF01454; MAGE; 1.
 PROSITE; PS00838; MAGE; 1.
 Antigen; Multigene family; Tumor antigen.
 DOMAIN 109 308 MAGE.
 FT DOMAIN 40 43 POLY-SER.
 FT MUTAGEN 170 170 V->D: IMPROVES ABILITY TO BIND TO HLA-A1.
 SQ SEQUENCE 314 AA; 35055 MW; 844F16335A2BCE7 CRC64;

Query Match 84.1%; Score 37; DB 1; Length 314;
 Best Local Similarity 77.8%; Pred. No. 2.7;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVAELVHFL 9
 Db 112 KVAELVHFL 120
 |. |||||
 |. |||||

RESULT 8
 MAG8_HUMAN
 ID MAG8_HUMAN STANDARD; PRT; 234 AA.
 AC P43361;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Melanoma-associated antigen 8 (MAGE-8 antigen).
 GN MAGEA8 OR MAGE8.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 (1)
 SEQUENCE FROM N.A.
 RP MEDLINE=95012457; PubMed=7927540;
 RA de Plaen E., Arden K., Traversari C., Gaforio J.J., Szikora J.-P.,
 de Smet C., Brasseur F., van der Bruggen P., Lethe B., Lurquin C.,
 Brasseur R., Chomez P., de Backer O., Cavenee W., Boon T.;
 RT "Structure, chromosomal localization, and expression of 12 genes of
 the MAGE family.";
 RL Immunogenetics 40:360-369(1994).


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DR InterPro; IPR001250; Man6p_isomerase1.
DR Pfam; PF01238; PMI_type1; 1.
DR PRINTS; PR00714; MAN6PISMRASE.
DR ProDom; PD004391; Man6p_isomerase1; 1.
DR TIGRfam; TIGR00218; manA; 1.
DR PROSITE; PS00965; PMI_I_1; 1.
DR PROSITE; PS00966; PMI_I_2; 1.
KW Isomerase; Zinc.
FT METAL 107 107 ZINC (BY SIMILARITY).
FT METAL 109 109 ZINC (BY SIMILARITY).
FT METAL 134 134 ZINC (BY SIMILARITY).
FT METAL 291 291 ZINC (BY SIMILARITY).
SQ SEQUENCE 461 AA; 50585 MW; 819F2BBA95D21006 CRC64;

Query Match 77.3%; Score 34; DB 1; Length 461;
Best Local Similarity 75.0%; Pred. No. 17;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VAELVHFL 9
Db 151 LAEIVHFL 158

RESULT 12
NIFA KLEOX
ID NIFA_KLEOX STANDARD; PRT; 524 AA.
AC P56266;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Nif-specific regulatory protein.
GN NIFA.
OS Klebsiella oxytoca.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Klebsiella.
OX NCBI_TaxID=571;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NG13;
RX MEDLINE=87115159; PubMed=3027503;
RA Kim Y.-M., Ahn K.-J., Beppu T., Uozumi T.;
RT "Nucleotide sequence of the nifLA operon of Klebsiella oxytoca NG13
and characterization of the gene products.";
RL Mol. Gen. Genet. 205:253-259(1986).
CC -!- FUNCTION: NIFA, A TRANSCRIPTIONAL ACTIVATOR, IS REQUIRED FOR
ACTIVATION OF MOST NIF OPERONS, WHICH ARE DIRECTLY INVOLVED IN
NITROGEN FIXATION. NIFA INTERACTS WITH SIGMA-54 (BY SIMILARITY).
CC -!- SIMILARITY: Contains 1 sigma-54 factor interaction ATP-binding
domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; D00339; BAA00245.1; -.
CC InterPro; IPR003593; AAA_ATPase.
CC InterPro; IPR008931; FIS-like.
CC InterPro; IPR003018; GAF.
CC InterPro; IPR002197; HTH_Fis.
CC InterPro; IPR002078; Sig54_interact.
CC Pfam; PF01590; GAF; 1.
CC Pfam; PF02954; HTH_8; 1.
CC Pfam; PF00158; Sigma54_activat; 1.
DR PRINTS; PR01590; HTHFIS.
DR SMART; SM00382; AAA; 1.
DR SMART; SM00065; GAF; 1.
DR TIGRfam; TIGR01199; HTH_fis; 1.
DR PROSITE; PS00675; SIGMA54_INTERACT_1; 1.
DR PROSITE; PS00676; SIGMA54_INTERACT_2; 1.

DR PROSITE; PS00688; SIGMA54_INTERACT_3; 1.
DR PROSITE; PS00445; SIGMA54_INTERACT_4; 1.
KW Nitrogen fixation; Transcription regulation; Activator;
KW ATP-binding; DNA-binding.
FT DOMAIN 1 182 A DOMAIN.
FT DOMAIN 212 481 SIGMA-54 FACTOR INTERACTION (POTENTIAL).
FT DOMAIN 482 524 C-TERMINAL DNA-BINDING DOMAIN.
FT NP_BIND 240 247 ATP (POTENTIAL).
FT NP_BIND 303 312 ATP (POTENTIAL).
FT DNA_BIND 496 515 H-T-H MOTIF (BY SIMILARITY).
SQ SEQUENCE 524 AA; 58650 MW; E0677A3605E6F9EE CRC64;

Query Match 77.3%; Score 34; DB 1; Length 524;
Best Local Similarity 75.0%; Pred. No. 20;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 VAELVHFL 9
Db 390 IAEIAHFL 397

RESULT 13
NIFA KLEPN
ID NIFA_KLEPN STANDARD; PRT; 524 AA.
AC P03027;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Nif-specific regulatory protein.
GN NIFA.
OS Klebsiella pneumoniae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Klebsiella.
OX NCBI_TaxID=573;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=89094839; PubMed=3062178;
RA Arnold W., Rump A., Klipp W., Priefer U.B., Puehler A.;
RT "Nucleotide sequence of a 24,206-base-pair DNA fragment carrying the
entire nitrogen fixation gene cluster of Klebsiella pneumoniae.";
RL J. Mol. Biol. 203:715-738(1988).
RN [2]
RP SEQUENCE FROM N.A.
RC MEDLINE=86220124; PubMed=3011408;
RA Drummond M., Whitty P., Wootton J.;
RT "Sequence and domain relationships of ntrC and nifA from Klebsiella
pneumoniae: homologues to other regulatory proteins.";
RL EMBO J. 5:441-447(1986).
RN [3]
RP SEQUENCE FROM N.A.
RC MEDLINE=85242120; PubMed=2989799;
RA Buikema W.J., Szeto W.W., Lemley P.V., Orme-Johnson W.H.,
RA Ausubel F.M.;
RT "Nitrogen fixation specific regulatory genes of Klebsiella pneumoniae
and Rhizobium meliloti share homology with the general nitrogen
regulatory gene ntrC of K. pneumoniae.";
RL Nucleic Acids Res. 13:4539-4555(1985).
CC -!- FUNCTION: NIFA, A TRANSCRIPTIONAL ACTIVATOR, IS REQUIRED FOR
ACTIVATION OF MOST NIF OPERONS, WHICH ARE DIRECTLY INVOLVED IN
NITROGEN FIXATION. NIFA INTERACTS WITH SIGMA-54.
CC -!- SIMILARITY: Contains 1 sigma-54 factor interaction ATP-binding
domain.
CC -----
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CC -----
CC AND IS SHORTER (484 AA) DUE TO A FRAMESHIFT.
CC -----
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DR EMBL; X02616; CAA26472.1; ALT_FRAME.
DR EMBL; X13303; CAA31682.1; -.
DR EMBL; X03580; CAA27260.1; -.
DR PIR; A91060; RGRBAP.
DR InterPro; IPR003593; AAA ATPase.
DR InterPro; IPR008931; FIS-like.
DR InterPro; IPR003018; GAF.
DR InterPro; IPR002197; HTH Fis.
DR InterPro; IPR002076; S1954_interact.
DR Pfam; PF01590; GAF; 1.
DR Pfam; PF02954; HTH 8; 1.
DR Pfam; PF00158; Sigma54 activat; 1.
DR PRINTS; PR01590; HTHFIS.
DR SMART; SM00382; AAA; 1.
DR SMART; SM00065; GAF; 1.
DR TIGRFAMs; TIGR01199; HTH_fis; 1.
DR PROSITE; PS00675; SIGMA54 INTERACT_1; 1.
DR PROSITE; PS00676; SIGMA54 INTERACT_2; 1.
DR PROSITE; PS00688; SIGMA54 INTERACT_3; 1.
DR PROSITE; PS50045; SIGMA54 INTERACT_4; 1.
KW Nitrogen fixation; Transcription regulation; Activator;
KW ATP-binding; DNA-binding.
FT DOMAIN 1 182 A DOMAIN.
FT DOMAIN 212 481 SIGMA-54 FACTOR INTERACTION (POTENTIAL).
FT DOMAIN 482 524 C-TERMINAL DNA-BINDING DOMAIN.
FT NP_BIND 240 247 ATP (POTENTIAL).
FT NP_BIND 303 312 ATP (POTENTIAL).
FT DNA_BIND 496 515 H-T-H MOTIF (BY SIMILARITY).
SQ SEQUENCE 524 AA; 58632 MW; F35B8511E580E5EB CRC64;

Query Match 77.3%; Score 34; DB 1; Length 524;
Best Local Similarity 75.0%; Pred. No. 20;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 VAEVHVEL 9
DB 390 IAEVHVEL 397

RESULT 14
TEGU HSVSA STANDARD; PRT; 2469 AA.
AC Q01056; 1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-APR-1993 (Rel. 25, Last annotation update)
DE Probable large tegument protein.
GN 64 OR ERF2.
OS Herpesvirus saimiri (strain 11).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Rhadinovirus.
OX NCBI_TaxID=10383;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92333686; PubMed=1321287;
RA Albrecht J.-C., Nicholas J., Biller D., Cameron K.R., Biesinger B.,
RA Newman C., Wittmann S., Craxton M.A., Coleman H., Fleckenstein B.,
RA Honess R.W.;
RT "Primary structure of the herpesvirus saimiri genome.";
RJ J. Virol. 66:5047-5058 (1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92230228; PubMed=1314457;
RA Nicholas J., Cameron K.R., Coleman H., Newman C., Honess R.W.;
RT "Analysis of nucleotide sequence of the rightmost 43 kbp of
RT herpesvirus saimiri (HVS) L-DNA: general conservation of genetic
RT organization between HVS and Epstein-Barr virus.";
RL Virology 188:296-310 (1992).
CC -!- SIMILARITY: Tegument protein.
CC -!- FUNCTION: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL36,
CC EHVS-1 24, EBV BPLF1, HVS-1 64, VZV 22, AND HCMV UL48.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; X64346; CAA45687.1; -.
DR EMBL; M86409; AAA46140.1; -.
DR InterPro; IPR006928; Herpes_teg_N.
DR Pfam; PF04843; Herpes teg N; 1.
SQ SEQUENCE 2469 AA; 280165 MW; D2B4B8DC08644CDB CRC64;

Query Match 77.3%; Score 34; DB 1; Length 2469;
Best Local Similarity 55.8%; Pred. No. 92;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVAELVHFL 9
DB 1521 RVTELHFI 1529

RESULT 15
YIMO YEAST STANDARD; PRT; 563 AA.
AC P40475; 1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypothetical 61.8 kDa protein in KGD1-SIM1 intergenic region.
GN YIL120W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RX MEDLINE=97313266; PubMed=9169870;
RA Churcher C.M., Bowman S., Badcock K., Bankier A., Brown D.,
RA Chillingworth T., Connor R., Devlin K., Gentles S., Hamlin N.,
RA Harris D.E., Horsnell T., Hunt S., Jagels K., Jones M., Lye G.,
RA Moule S., Odell C., Pearson D., Rajandream M.A., Rice P., Rowley N.,
RA Skelton J., Smith V., Walsh S., Whitehead S., Barrell B.G.;
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome IX.";
RL Nature 387:84-87 (1997).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC -!- SIMILARITY: BELONGS TO THE MAJOR FACILITATOR FAMILY (ALSO KNOWN
CC AS THE DRUG RESISTANCE TRANSLUCASE FAMILY). BELONGS TO THE
CC CARI/CYHR SUBFAMILY.
CC -----
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CC -----
DR EMBL; Z46833; CAA86872.1; -.
DR PIR; S49889; S49889.
DR Germline; 139655; -.
DR SGD; S0001382; YIL120W.
DR GO; GO:0005886; C:plasma membrane; IDA.
DR GO; GO:0006855; P:multidrug transport; IMP.
DR InterPro; IPR007114; MFS.
DR InterPro; IPR005828; Sub_transporter.
DR Pfam; PF00083; sugar_tr; 1.
DR PROSITE; PS50850; MFS; 1.
KW Hypothetical protein; Transport; Transmembrane.
FT TRANSMEM 76 96 POTENTIAL.
FT TRANSMEM 109 129 POTENTIAL.
FT TRANSMEM 136 156 POTENTIAL.

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FT TRANSMEM 166 186 POTENTIAL.
FT TRANSMEM 196 216 POTENTIAL.
FT TRANSMEM 225 245 POTENTIAL.
FT TRANSMEM 297 317 POTENTIAL.
FT TRANSMEM 342 362 POTENTIAL.
FT TRANSMEM 422 442 POTENTIAL.
FT TRANSMEM 446 466 POTENTIAL.
FT TRANSMEM 482 502 POTENTIAL.
FT TRANSMEM 512 532 POTENTIAL.
SQ SEQUENCE 563 AA; 61758 MW; 5FD8A6F9F7C71C72 CRC64;

Query Match 75.0%; Score 33; DB 1; Length 563;
Best Local Similarity 85.7%; Pred. No. 34;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVAELVH 7
Db 399 KVAELIH 405

RESULT 16
NUSC_MAIZE STANDARD; PRT; 738 AA.
AC P46620;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE NAD(P)H-quinone oxidoreductase chain 5, chloroplast (EC 1.6.5.-)
DE NAD(P)H dehydrogenase, chain 5) (NADH-plastoquinone oxidoreductase chain 5).
DE NDHF OR NDH5.
OS Zea mays (Maize).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95395841; PubMed=7666415;
RA Maier R.M., Neckermann K., Igloi G.L., Koessel H.;
RT "Complete sequence of the maize chloroplast genome: gene content,
RT hotspots of divergence and fine tuning of genetic information by
RT transcript editing."
RL J. Mol. Biol. 251:614-628 (1995).
RN [2]
RP SEQUENCE OF 9-709 FROM N.A.
RC Trisub-Leaf;
RA Clark L.G., Zhang W., Wendel J.F.;
RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: NAD(P)H + plastoquinone = NAD(P) (+) +
CC plastoquinol.
CC
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CC
CC EMBL; X86563; CAA60346.1; -.
CC DR EMBL; U21985; AAA64703.1; -.
CC DR PIR; S58612; S58612.
CC DR Gramene; P46620; -.
CC DR MaizeDB; 107782; -.
CC DR InterPro; IPR003916; NADH_oxred5.
CC DR InterPro; IPR001750; Oxidored_q1.
CC DR InterPro; IPR002128; Oxidored_q1_C.
CC DR InterPro; IPR001516; Oxidored_q1_N.
CC DR Pfam; PF00361; oxidored_q1; 1.
CC DR Pfam; PF01010; oxidored_q1_C; 1.
CC DR Pfam; PF00662; oxidored_q1_N; 1.
CC
CC EMBL; X86563; CAA60346.1; -.
CC DR EMBL; U21985; AAA64703.1; -.
CC DR PIR; S58612; S58612.
CC DR Gramene; P46620; -.
CC DR MaizeDB; 107782; -.
CC DR InterPro; IPR003916; NADH_oxred5.
CC DR InterPro; IPR001750; Oxidored_q1.
CC DR InterPro; IPR002128; Oxidored_q1_C.
CC DR InterPro; IPR001516; Oxidored_q1_N.
CC DR Pfam; PF00361; oxidored_q1; 1.
CC DR Pfam; PF01010; oxidored_q1_C; 1.
CC DR Pfam; PF00662; oxidored_q1_N; 1.

DR PRINTS; PR01434; NADHDHGNASE5.
KW Oxidoreductase; NAD; NADP; Quinone; Plastoquinone; Chloroplast.
FT CONFLICT 268 268 MISSING (IN REF. 2).
FT CONFLICT 289 289 W -> L (IN REF. 2).
FT CONFLICT 570 570 R -> G (IN REF. 2).
FT CONFLICT 680 680 K -> R (IN REF. 2).
SQ SEQUENCE 738 AA; 82976 MW; F4E3EBD0DD3C91FA CRC64;

Query Match 75.0%; Score 33; DB 1; Length 738;
Best Local Similarity 75.0%; Pred. No. 45;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVAELVHF 8
Db 680 KLAELTHF 687

RESULT 17
NUSC_DAMDI STANDARD; PRT; 744 AA.
AC Q32126;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE NAD(P)H-quinone oxidoreductase chain 5, chloroplast (EC 1.6.5.-)
DE (NAD(P)H dehydrogenase, chain 5) (NADH-plastoquinone oxidoreductase chain 5).
DE NDHF.
GN Dampiera diversifolia.
OS Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC campanulids; Asterales; Goodeniaceae; Dampiera.
OX NCBI_TaxID=41565;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96036088; PubMed=7479789;
RA Kim K.-J., Jansen R.K.;
RT "ndhF sequence evolution and the major clades in the sunflower
RT family."
RL Proc. Natl. Acad. Sci. U.S.A. 92:10379-10383 (1995).
CC -!- CATALYTIC ACTIVITY: NAD(P)H + plastoquinone = NAD(P) (+) +
CC plastoquinol.
CC
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CC
CC EMBL; L39386; AAC37742.1; -.
CC DR PIR; T13043; T13043.
CC DR InterPro; IPR003916; NADH_oxred5.
CC DR InterPro; IPR001750; Oxidored_q1.
CC DR InterPro; IPR002128; Oxidored_q1_C.
CC DR InterPro; IPR001516; Oxidored_q1_N.
CC DR Pfam; PF00361; oxidored_q1; 1.
CC DR Pfam; PF01010; oxidored_q1_C; 1.
CC DR Pfam; PF00662; oxidored_q1_N; 1.
CC
CC EMBL; L39386; AAC37742.1; -.
CC DR PIR; T13043; T13043.
CC DR InterPro; IPR003916; NADH_oxred5.
CC DR InterPro; IPR001750; Oxidored_q1.
CC DR InterPro; IPR002128; Oxidored_q1_C.
CC DR InterPro; IPR001516; Oxidored_q1_N.
CC DR Pfam; PF00361; oxidored_q1; 1.
CC DR Pfam; PF01010; oxidored_q1_C; 1.
CC DR Pfam; PF00662; oxidored_q1_N; 1.
CC
CC EMBL; X86563; CAA60346.1; -.
CC DR EMBL; U21985; AAA64703.1; -.
CC DR PIR; S58612; S58612.
CC DR Gramene; P46620; -.
CC DR MaizeDB; 107782; -.
CC DR InterPro; IPR003916; NADH_oxred5.
CC DR InterPro; IPR001750; Oxidored_q1.
CC DR InterPro; IPR002128; Oxidored_q1_C.
CC DR InterPro; IPR001516; Oxidored_q1_N.
CC DR Pfam; PF00361; oxidored_q1; 1.
CC DR Pfam; PF01010; oxidored_q1_C; 1.
CC DR Pfam; PF00662; oxidored_q1_N; 1.

Query Match 75.0%; Score 33; DB 1; Length 744;
Best Local Similarity 75.0%; Pred. No. 45;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVAELVHF 8
Db 682 KLAELTHF 689
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RESULT 18
SUS2_ARATH
ID SUS2_ARATH STANDARD; PRT; 805 AA.
AC Q00917; Q9FJ20;
DT 01-APR-1993 (Rel. 25, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Sucrose synthase (EC 2.4.1.13) (Sucrose-UDP glucosyltransferase).
GN AT5G49190 OR K2IP3.6.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eumecids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=92119221; PubMed=1531031;
RA Chopra S., Del-Favero J., Dolferus R., Jacobs M.;
RT "Sucrose synthase of Arabidopsis: genomic cloning and sequence
characterization.";
RL Plant Mol. Biol. 18:131-134(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=99158233; PubMed=10048488;
RA Asamizu E., Sato S., Kaneko T., Nakamura Y., Kotani H., Miyajima N.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. VIII.
Sequence features of the regions of 1,081,958 bp covered by seventeen
physically assigned P1 and TAC clones.";
RL DNA Res. 5:379-391(1998).
CC -1- FUNCTION: Sucrose-cleaving enzyme that provides UDP-glucose and
fructose for various metabolic pathways.
CC -1- CATALYTIC ACTIVITY: UDP-glucose + D-fructose = UDP + sucrose.
CC -1- INDUCTION: By anaerobic stress.
CC -1- SIMILARITY: Belongs to the glycosyltransferase family 1. Plant
sucrose synthase subfamily.
CC -1- CAUTION: Ref.1 sequence differs from that shown due to frameshifts
in positions 9 and 12.
CC -----
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CC -----
DR EMBL; X60987; CAA43303.1; ALT FRAME.
DR EMBL; AB016872; BAB10337.1; -.
DR InterPro; IPR001296; Glyco trans 1.
DR InterPro; IPR000368; Sucrose synth.
DR Pfam; PF00534; Glycos_transf_1; 1.
DR Pfam; PF00862; Sucrose_synth; 1.
DR Transferase; Glycosyltransferase; Multigene family.
FT CONFLICT 35 35 Q -> H (IN REF. 1).
FT CONFLICT 133 133 D -> H (IN REF. 1).
FT CONFLICT 156 157 FL -> LV (IN REF. 1).
FT CONFLICT 281 282 PH -> RY (IN REF. 1).
FT CONFLICT 286 286 G -> A (IN REF. 1).
FT CONFLICT 298 298 G -> A (IN REF. 1).
FT CONFLICT 648 648 A -> V (IN REF. 1).
FT CONFLICT 718 723 ATLVSF -> GSLAL (IN REF. 1).
SQ SEQUENCE 805 AA; 92007 MW; 448F92326CCA755E CRC64;

Query Match 75.0%; Score 33; DB 1; Length 805;
Best Local Similarity 66.7%; Pred. No. 49;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVALLVHFL 9
|||:|:|

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Db 243 KVSEMVHLL 251

RESULT 19
ALF1_BACSU
ID ALF1_BACSU STANDARD; PRT; 285 AA.
AC P13243;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Probable fructose-bisphosphate aldolase 1 (EC 4.1.2.13).
GN FBAA OR FBA OR FBA1 OR TSR OR BSU37120.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168 / JH642;
RX MEDLINE=88314920; PubMed=2457578;
RA Trach K., Chapman J.W., Piggot P., Lecoq D., Hoch J.A.;
RT "Complete sequence and transcriptional analysis of the spoOF region
of the Bacillus subtilis chromosome.";
RL J. Bacteriol. 170:4194-4208(1988).
RN [2]
RP REVISIONS, AND SEQUENCE OF 1-26 FROM N.A.
RC STRAIN=168 / JH642;
RX MEDLINE=92349962; PubMed=1640835;
RA Mitchell C., Morris P.W., Lum L., Spiegelman G., Vary J.C.;
RT "The amino acid sequence of a Bacillus subtilis phosphoprotein that
matches an orfV-tsr coding sequence.";
RL Mol. Microbiol. 6:1345-1349(1992).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98015417; PubMed=9353933;
RA Pressac E., Moszer I., Boursier L., Cruz Ramos H.C., De La Fuente V.,
RA Hullo M.-F., Lelong C., Schleich S., Sekowska A., Song B.H.,
RA Villani G., Kunst F., Danchin A., Glaser P.;
RT "The Bacillus subtilis genome from gerBC (311 degrees) to licR (334
degrees).";
RL Microbiology 143:3313-3328(1997).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Betero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borries R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Guisepi G., Glaser P., Goffeau A., Colightly E.J., Grandi G.,
RA Halbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Pressac E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Sorokin A., Taccioni E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;

```

RT "The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.";
 RL Nature 390:249-256 (1997).
 RN [5]
 RP SEQUENCE OF 1-16, AND PHOSPHORYLATION.
 RX MEDLINE=92210489; PubMed=1556067;
 RA Mitchell C., Morris P.W., Vary J.C.;
 RT "Identification of proteins phosphorylated by ATP during sporulation
 of *Bacillus subtilis*.";
 RL J. Bacteriol. 174:2474-2477 (1992).
 CC -|- CATALYTIC ACTIVITY: D-fructose 1,6-bisphosphate = glycerone
 phosphate + D-glyceraldenhyde 3-phosphate.
 CC -|- COFACTOR: Zinc.
 CC -|- PATHWAY: Glycolysis; sixth step.
 CC -|- SIMILARITY: Belongs to class II fructose-bisphosphate aldolase
 family.
 CC -----
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 CC -----
 DR EMBL; M22039; AAA16803.1; -;
 DR EMBL; S42590; AAB22716.1; -;
 DR EMBL; Z49782; CAB89873.1; -;
 DR EMBL; Z99122; CAB15729.1; -;
 DR PIR; S55426; D32354.
 DR HSSP; P11604; 1B57.
 DR Subtilisin; BG10412; fbaA.
 DR InterPro; IPR000771; K_bp_aldolase.
 DR Pfam; PF01116; F_bp_aldolase; 1.
 DR ProDom; PD002376; K_bp_aldolase; 1.
 DR TricRams; TricR00167; cdbA; 1.
 DR PROSITE; PS00602; ALDOLASE CLASS II.1; 1.
 DR PROSITE; PS00806; ALDOLASE CLASS II.2; 1.
 DR Lysase; Glycolysis; Zinc; phosphorylation; Complete proteome.
 KW METAL 83 ZINC (BY SIMILARITY).
 FT METAL 86 86 ZINC (BY SIMILARITY).
 SQ SEQUENCE 285 AA; 30400 MW; 482D3CE048583BCF CRC64;
 Query Match 72.7%; Score 32; DB 1; Length 285;
 Best Local Similarity 75.0%; Pred. No. 28;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 KVAELVHF 8
 Db 122 KVELAHF 129
 RESULT 20
 RECF_ECOLI STANDARD; PRT; 356 AA.
 ID AC P03016;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE DNA replication and repair protein recF.
 GN RECF OR UVRF OR B3700 OR C4622 OR Z5191 OR ECS4635.
 OS *Escherichia coli*,
 OS *Escherichia coli* O6, and
 OS *Escherichia coli* O157:H7.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; *Escherichia*.
 CX NCBI_TaxID=562, 217992, 83334;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=84272685; PubMed=6379647;
 RA Blaser M.A., Sandler S.J., Armengod M.-E., Ream L.W., Clark A.J.;
 RT "Molecular analysis of the recF gene of *Escherichia coli*.";
 Proc. Natl. Acad. Sci. U.S.A. 81:4622-4626 (1984).

RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE=84297235; PubMed=6089112;
 RA Adachi T., Mizuuchi K., Menzel R., Gellert M.;
 RT "DNA sequence and transcription of the region upstream of the *E. coli*
gyrB gene.";
 RL Nucleic Acids Res. 12:6389-6395 (1984).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12 / MG1655;
 RX MEDLINE=93315143; PubMed=7686882;
 RA Burland V.D., Plunkett G. III, Daniels D.L., Blattner F.R.;
 RT "DNA sequence and analysis of 136 kilobases of the *Escherichia coli*
 genome: organizational symmetry around the origin of replication.";
 RL Genomics 16:551-561 (1993).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=O6:H1 / CFT073 / ATCC 700928;
 RX MEDLINE=22388234; PubMed=12471157;
 RA Welch R.A., Buckland V., Plunkett G. III, Redford P., Roesch P.,
 Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
 Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
 Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
 RT "Extensive mosaic structure revealed by the complete genome sequence
 of uropathogenic *Escherichia coli*.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=O157:H7 / EDL933 / ATCC 700927;
 RX MEDLINE=21074935; PubMed=11206551;
 RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
 Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
 Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
 Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamoudis K.,
 Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
 Welch R.A., Blattner F.R.;
 RT "Genome sequence of enterohaemorrhagic *Escherichia coli* O157:H7.";
 RL Nature 409:529-533 (2001).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=O157:H7 / RMD 0509952;
 RX MEDLINE=21156231; PubMed=11258796;
 RA Hayaishi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
 Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
 Iida T., Takami H., Honda T., Sakakawa C., Ogasawara N., Yasunaga T.,
 Kihara S., Shiba T., Hattori M., Shinagawa H.;
 RT "Complete genome sequence of enterohaemorrhagic *Escherichia coli*
 O157:H7 and genomic comparison with a laboratory strain K-12.";
 RL DNA Res. 8:11-22 (2001).
 RN [7]
 RP SEQUENCE OF 1-12, AND DNA-BINDING.
 RX MEDLINE=91035238; PubMed=2228960;
 RA Griffin T.J. IV, Kolodner R.D.;
 RT "Purification and preliminary characterization of the *Escherichia*
coli K-12 recF protein.";
 RL J. Bacteriol. 172:6291-6299 (1990).
 RN [8]
 RP MUTAGENESIS OF LYS-35.
 RX MEDLINE=92178981; PubMed=1542576;
 RA Sandler S.J., Chackerian B., Li J.T., Clark A.J.;
 RT "Sequence and complementation analysis of recF genes from *Escherichia*
coli, *Salmonella typhimurium*, *Pseudomonas putida* and *Bacillus*
subtilis: evidence for an essential phosphate binding loop.";
 RL Nucleic Acids Res. 20:839-845 (1992).
 CC -|- FUNCTION: The recF protein is involved in DNA metabolism; it is
 required for DNA replication and normal SOS inducibility. RecF
 binds preferentially to single-stranded, linear DNA. It also seems
 to bind ATP.
 CC -|- SUBCELLULAR LOCATION: Cytoplasmic (potential).
 CC -|- SIMILARITY: Belongs to the recF family.
 CC -----
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 CC -----
 DR EMBL; K02179; AAA24511.1; -;
 DR EMBL; X04341; CAA27870.1; -;
 DR EMBL; LI0328; AAG62051.1; -;
 DR EMBL; AE000447; AAC76723.1; -;
 DR EMBL; AE016769; AAN83055.1; -;
 DR EMBL; AE005601; AAG58897.1; -;
 DR EMBL; AP002566; BAB38058.1; -;
 DR PIR; A03547; RQECF.
 DR PIR; C91208; C91208.
 DR PIR; E86054; E86054.
 DR EcoGene; EG10828; recF.
 DR HAMAP; MF_00365; -; 1.
 DR InterPro; IPR001238; RecF.
 DR InterPro; IPR003395; SMC_N.
 DR InterPro; IPR002017; Spectrin.
 DR Pfam; PF02463; SMC_N; 1.
 DR TIGRFAMs; TIGR00611; recF; 1.
 DR PROSITE; PS00617; REC_F_1; 1.
 DR PROSITE; PS00618; REC_F_2; 1.
 DR DNA damage; DNA replication; SOS response; DNA repair;
 KW ATP-binding; Complete proteome.
 FT INIT MET 0
 FT NP_BIND 29 36 ATP (POTENTIAL).
 FT MUTAGEN 35 35 K->R; WEAKLY ACTIVE.
 FT MUTAGEN 35 35 K->R; WEAKLY ACTIVE.
 SQ SEQUENCE 356 AA; 40382 MW; 1EF155B2BD302776 CRC64;
 Query Match 72.7%; Score 32; DB 1; Length 356;
 Best Local Similarity 66.7%; Pred. No. 35;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 KVAELVHFL 9
 DB 103 KVAELAHLM 111
 RESULT 21
 TRD2 ANASP
 ID TRD2 ANASP STANDARD; PRT; 362 AA.
 AC Q8YXQ9;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Anthranilate phosphoribosyltransferase 2 (EC 2.4.2.18).
 GN TRPD2 OR ALR1153.
 OS Anabaena sp. (strain PCC 7120).
 OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
 OX NCBI_TaxID=103690;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21595285; PubMed=11759840;
 RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
 RA Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
 RA Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
 RA Yasuda M., Tabata S.;
 RT "Complete genomic sequence of the filamentous nitrogen-fixing
 cyanobacterium Anabaena sp. strain PCC 7120.";
 RL DNA Res. 8:205-213(2001).
 CC -1- CATALYTIC ACTIVITY: Anthranilate + phosphoribosyldiphosphate =
 CC N-5'-phosphoribosyl-anthranilate + diphosphate.
 CC -1- PATHWAY: Tryptophan biosynthesis; second step.
 CC -1- SIMILARITY: Belongs to the anthranilate phosphoribosyltransferase
 CC family.
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 CC -----
 DR EMBL; AP003584; BAB73110.1; -;
 DR PIR; AP1950; AFI950.
 DR HAMAP; MF_00211; -; 1.
 DR InterPro; IPR005940; Ant_phospho_trans.
 DR InterPro; IPR003112; Glyco_trans_3.
 DR Pfam; PF02885; Glycos_trans_3N; 1.
 DR Pfam; PF00591; Glycos_trans_3; 1.
 DR ProDom; PD001864; Glyco_trans_3; 1.
 DR TIGRFAMs; TIGR01245; trpb; 1.
 DR Tryptophan biosynthesis; Transferase; Glycosyltransferase;
 KW Complete proteome.
 SQ SEQUENCE 362 AA; 37597 MW; C392D1446391AC13 CRC64;
 Query Match 72.7%; Score 32; DB 1; Length 362;
 Best Local Similarity 66.7%; Pred. No. 36;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KVAELVHFL 9
 DB 352 KLAQLVYFL 360
 RESULT 22
 TYPH MYCPN
 ID TYPH MYCPN STANDARD; PRT; 421 AA.
 AC P75052;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Thymidine phosphorylase (EC 2.4.2.4) (TDRPase).
 GN DSOA OR MPN064 OR MP090.
 OS Mycoplasma pneumoniae.
 OC Bacteria; Firmicutes; Mollicutes; Mycoplaemataceae; Mycoplasma.
 OX NCBI_TaxID=2104;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 29342 / ML29;
 RX MEDLINE=97105885; PubMed=8948633;
 RA Himmelfreich R., Hilbert H., Plagens H., Pirkel E., Li B.-C.,
 RA Herrmann R.;
 RT "Complete sequence analysis of the genome of the bacterium Mycoplasma
 pneumoniae";
 RL Nucleic Acids Res. 24:4420-4449(1996).
 CC -1- FUNCTION: THE ENZYMES WHICH CATALYZE THE REVERSIBLE PHOSPHORYLOSIS
 CC OF PYRIMIDINE NUCLEOSIDES ARE INVOLVED IN THE DEGRADATION OF THESE
 CC COMPOUNDS AND IN THEIR UTILIZATION AS CARBON AND ENERGY SOURCES,
 CC OR IN THE RESCUE OF PYRIMIDINE BASES FOR NUCLEOTIDE SYNTHESIS.
 CC -1- CATALYTIC ACTIVITY: Thymidine + phosphate = thymine + 2-deoxy-D-
 CC ribose 1-phosphate.
 CC -1- SUBUNIT: Homodimer (By similarity).
 CC -1- SIMILARITY: Belongs to the thymidine/pyrimidine-nucleoside
 CC phosphorylase family.
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 CC -----
 DR EMBL; AE000011; AAB95738.1; -;
 DR PIR; S73416; S73416.
 DR HGSP; P77836; IBRW.
 DR InterPro; IPR000312; Glyco_trans_3.
 DR InterPro; IPR000053; Thymid_phosphis.
 DR Pfam; PF02885; Glycos_trans_3N; 1.

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DR Pfam; PF00591; Glycos_transf_3; 1.
DR PIRSF; PIRSF000478; Thymid_phosphils; 1.
DR ProDom; PD001864; Glyco trans 3; 1.
DR ProDom; PD005916; Thymid_phosphils; 1.
DR PROSITE; PS00647; THYMID_PHOSPHORYLASE; 1.
KW Transferase; Glycosyltransferase; Complete proteome.
SQ SEQUENCE 421 AA; 46628 MW; E29DBF93C6D8549F CRC64;

Query Match 72.7%; Score 32; DB 1; Length 421;
Best Local Similarity 66.7%; Pred. No. 42;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVLELVHFL 9
Db 251 EVLEVVHFL 259

RESULT 23
TRME MYCPN STANDARD; PRT; 442 AA.
AC P75104;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Probable tRNA modification GTPase trmE.
GN TRME OR THDF OR MPN008 OR MP146.
OS Mycoplasma pneumoniae.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2104;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 29342 / M129;
RX MEDLINE=97105885; PubMed=8948633;
RA Himmelreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
RA Hermann R.;
RT "Complete sequence analysis of the genome of the bacterium Mycoplasma
RT pneumoniae.";
RL Nucleic Acids Res. 24:4420-4449(1996).
CC -!- FUNCTION: Exhibits a very high intrinsic GTPase hydrolysis rate.
CC Involved in the biosynthesis of the hypermodified nucleoside 5-
CC methylaminomethyl-2-thiouridine, which is found in the wobble
CC position of some tRNAs (By similarity).
CC -!- SIMILARITY: Belongs to the era/trmE family of GTP-binding
CC proteins. TrmE subfamily.
CC
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CC
CC EMBL; AE000016; AAB95794.1; -.
CC F1R; S73472; S73472.
CC HAMAP; MF 00379; -.
CC InterPro; IPR005289; GTP-binding_dom.
CC InterPro; IPR006073; GTP1_OBG.
CC InterPro; IPR002917; MWR_HSR1.
CC InterPro; IPR001806; Rast_transfrmng.
CC InterPro; IPR005225; Small_GTP.
CC InterPro; IPR004520; TrdF.
CC Pfam; PF01926; MWR_HSR1; 1.
CC PRINTS; PR00326; GTP1_OBG.
CC PRINTS; PR00449; RASTRNSFRMNG.
CC TIGRFAMs; TIGR00650; MG442; 1.
CC TIGRFAMs; TIGR00231; small_GTP; 1.
CC TIGRFAMs; TIGR00450; trdF; 1.
CC TRNA processing; GTP-binding; Complete proteome.
KW NP_BIND 224 231 GTP (POTENTIAL).
FT NP_BIND 271 275 GTP (POTENTIAL).
FT NP_BIND 331 334 GTP (POTENTIAL).
SQ SEQUENCE 442 AA; 49780 MW; FA8849BA0BCB9AD5 CRC64;
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Query Match 72.7%; Score 32; DB 1; Length 442;
Best Local Similarity 75.0%; Pred. No. 44;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 VAEVLHFL 9
Db 388 IAELEHFL 395

RESULT 24
PUR8_HAEIN STANDARD; PRT; 456 AA.
AC P44787;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Adenylosuccinate lyase (EC 4.3.2.2) (Adenylosuccinase) (ASL).
GN PUR8 OR HI0639.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Rd / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Keiley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Uterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
RT Rd.";
RL Science 269:496-512(1995).
CC -!- CATALYTIC ACTIVITY: N(6)-(1,2-dicarboxylethyl)AMP = fumarate + AMP.
CC -!- CATALYTIC ACTIVITY: (S)-2-[5-amino-1-(5-phospho-D-
CC ribosyl)imidazole-4-carboxamido]succinate = fumarate + 5-amino-1-
CC (5-phospho-D-ribosyl)imidazole-4-carboxamide.
CC -!- PATHWAY: De novo purine biosynthesis; eighth step.
CC -!- SIMILARITY: Belongs to the lyase 1 family. Adenylosuccinate lyase
CC subfamily.
CC
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CC
CC EMBL; U32747; AAC22299.1; -.
CC TIGR; HI0639; -.
CC InterPro; IPR000362; Fumarate lyase.
CC InterPro; IPR008948; L-Aspartase-like.
CC InterPro; IPR004769; Pur lyase.
CC Pfam; PF00206; lyase_1; 1.
CC PRINTS; PR00149; FUMRATLYASE.
CC TIGRFAMs; TIGR00928; purB; 1.
CC PROSITE; PS00163; FUMARATE_LYASES; 1.
CC Purine biosynthesis; Lyase; Complete proteome.
FT ACT_SITE 91 91 ACID (BY SIMILARITY).
FT ACT_SITE 171 171 BASE (BY SIMILARITY).
SQ SEQUENCE 456 AA; 93021D612A3CAC8 CRC64;

Query Match 72.7%; Score 32; DB 1; Length 456;
Best Local Similarity 62.5%; Pred. No. 45;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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QY 1 KVAELVHF 8
Db 112 KVSEFIHF 119

RESULT 25
RBF1 CANAL
ID _RBF1 CANAL STANDARD; PRT; 527 AA.
AC Q00312;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Transcription factor RBF1 (RPG-box-binding factor) (Repressor-
DE activator protein 1).
GN RBF1.
OS Candida albicans (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=5476;
RN [1]
SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=ATCC 10231;
RX MEDLINE=97195786; PubMed=9043119;
RA Iehii N., Yamamoto M., Lahm H.-W., Izumi S., Yoshihara F.,
RA Nakayama H., Arisawa M., Aoki Y.;
RT "A DNA-Binding protein from Candida albicans that binds to the RPG
RT box of Saccharomycetes cerevisiae and the telomeric repeat sequence of
RT C. albicans.";
RL Microbiology 143:417-427(1997).
RN [2]
CHARACTERIZATION.
RX MEDLINE=97195789; PubMed=9043120;
RA Iehii N., Yamamoto M., Yoshihara F., Arisawa M., Aoki Y.;
RT "Biochemical and genetic characterization of Rbf1p, a putative
RT transcription factor of Candida albicans.";
RL Microbiology 143:429-435(1997)
CC -!- FUNCTION: Transcriptional activator that binds to the RPG box and
CC to telomeres. May be involved in the regulation of the transition
CC between yeast and filamentous forms at the level of transcription.
CC -!- SUBCELLULAR LOCATION: Nuclear; predominantly.
CC
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CC
CC EMBL; D85862; BAA12888.1; -.
CC Transcription regulation; DNA-binding; Activator; Nuclear protein;
CC Telomere.
KW
FT DNA BIND 160 300 POTENTIAL.
FT DOMAIN 73 80 POLY-ALA.
FT DOMAIN 135 139 POLY-GLN.
FT DOMAIN 326 329 POLY-HIS.
FT DOMAIN 332 353 POLY-GLN.
FT DOMAIN 398 405 POLY-GLN.
FT DOMAIN 445 452 POLY-ALA.
FT DOMAIN 478 481 POLY-GLN.
SQ SEQUENCE 527 AA; 59441 MW; ADD675F937A807D CRC64;

Query Match 72.7%; Score 32; DB 1; Length 527;
Best Local Similarity 85.7%; Pred. No. 52;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 AELVHFL 9
Db 193 AELVHFV 199

RESULT 26
IRAL MOUSE
```



```
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding.
FT DOMAIN 212 521 PROTEIN KINASE.
FT NP BIND 218 226 ATP (BY SIMILARITY).
FT BINDING 239 239 ATP (BY SIMILARITY).
FT ACT SITE 338 BY SIMILARITY.
SQ SEQUENCE 710 AA; 77269 MW; 8A501F002CD3EBD2 CRC64;

Query Match 72.7%; Score 32; DB 1; Length 710;
Best Local Similarity 66.7%; Pred. No. 70;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVAVLVHFL 9
Db 79 RVADLVHIL 87

RESULT 27
ID _IRAI_HUMAN STANDARD; PRT; 712 AA.
AC PS1617;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Interleukin-1 receptor-associated kinase 1 (EC 2.7.1.-) (IRAK-1).
GN IRAK1 OR IRAK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=96186673; PubMed=8599092;
RA Cao Z., Henzel W.J., Gao X.;
RT "IRAK: a kinase associated with the interleukin-1 receptor.";
RL Science 271:1128-1131(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Platzter M., Bauer D., Drescher B.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Reichwald K., Kioschis P., Rosenthal A., Platzter M.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP INTERACTION WITH PELI1.
RX MEDLINE=22538429; PubMed=12496252;
RA Jiang Z., Johnson H.J., Nie H., Qin J., Bird T.A., Li X.;
RT "Pellino 1 is required for interleukin-1 (IL-1)-mediated signaling
RT through its interaction with the IL-1 receptor-associated kinase 4
RT (IRAK4)-IRAK-tumor necrosis factor receptor-associated factor 6
RT (TRAF6) complex.";
RL J. Biol. Chem. 278:10952-10956(2003).
RN [5]
RP INTERACTION WITH PELI2.
RX MEDLINE=2274764; PubMed=12860405;
RA Strelow A., Kollweh C., Wesche H.;
RT "Characterization of Pellino2, a substrate of IRAK1 and IRAK4.";
RL FEBS Lett. 547:157-161(2003).
RN [6]
RP INTERACTION WITH PELI3.
RX MEDLINE=22756745; PubMed=12874243;
RA Jensen L.E., Whitehead A.S.;
RT "Pellino3, a novel member of the Pellino protein family, promotes
RT activation of c-Jun and Elk-1 and may act as a scaffolding protein.";
RL J. Immunol. 171:1500-1506(2003).
CC -!- FUNCTION: Involved in IL-1 pathway. This kinase associates with
CC the IL-1 receptor IL1R-1. This association is rapid and IL-1
CC dependent.
CC -!- SUBUNIT: Found in a complex containing TRAF6, PELI1 and IRAK4.
CC Interacts with PELI2 and PELI3.
CC
```

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CC -!- TISSUE SPECIFICITY: Seems to be ubiquitous, although present in
CC small amounts.
CC -!- PTM: An extensive phosphorylation of IRAK occurs after its
CC association with IL1R-1. This step could be linked to the
CC activation of the kinase.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC PELLE SUBFAMILY.
CC
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CC
CC -----
CC EMBL; L76191; AAC41949.1; -
CC EMBL; U52112; -; NOT_ANNOTATED_CDS.
CC EMBL; AF030876; AAC08756.1; -
CC FIR; G02512; G02512.
CC Genew; HGNC:6112; IRAK1.
CC MIM; 300283; -
CC GO; GO:0045323; C:interleukin-1 receptor complex; NAS.
CC GO; GO:0004704; F:INF-kappaB-inducing kinase activity; TAS.
CC GO; GO:0005515; F:protein binding; ISS.
CC GO; GO:0006468; P:protein amino acid phosphorylation; TAS.
CC GO; GO:0007165; P:signal transduction; NAS.
CC InterPro; IPR000488; Death.
CC InterPro; IPR000719; Prot kinase.
CC InterPro; IPR008271; Ser_thr_kin_AS.
CC Pfam; PF00531; death; 1.
CC Pfam; PF00069; pkinase; 1.
CC ProDom; PD00001; Prot kinase; 1.
CC PROSITE; PS00107; PROTEIN KINASE ATP; 1.
CC PROSITE; PS00108; PROTEIN KINASE ST; 1.
CC PROSITE; PS00111; PROTEIN KINASE DOM; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding.
FT DOMAIN 212 521 PROTEIN KINASE.
FT NP BIND 218 226 ATP (BY SIMILARITY).
FT BINDING 239 239 ATP (BY SIMILARITY).
FT ACT SITE 338 BY SIMILARITY.
FT CONFLICT 196 196 F -> S (IN REF. 1).
FT CONFLICT 532 532 S -> L (IN REF. 1).
SQ SEQUENCE 712 AA; 76536 MW; A7ADE75D3A3981D CRC64;

Query Match 72.7%; Score 32; DB 1; Length 712;
Best Local Similarity 66.7%; Pred. No. 70;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVAVLVHFL 9
Db 79 RVADLVHIL 87

RESULT 28
EPS8_HUMAN STANDARD; PRT; 822 AA.
ID EPS8_HUMAN STANDARD; PRT; 822 AA.
AC Q12929;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Epidermal growth factor receptor kinase substrate EPS8.
GN EPS8.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94366758; PubMed=8084614;
RA Hong W.T., Carlomagno F., Druck T., Barletta C., Croce C.M.,
RA Huebner K., Kraus M.H., di Fiore P.P.;
RT "Evolutionary conservation of the EPS8 gene and its mapping to human
```


RT chromosome 12q23-q24.";
 RL Oncogene 9:3057-3061(1994).
 CC -1- FUNCTION: Upon binding to EGF receptor enhances EGF-dependent
 CC mitogenic signals. Can bind multiple cellular targets.
 CC -1- TISSUE SPECIFICITY: Expressed in all tissues analyzed, including
 CC heart, brain, placenta, lung, liver, skeletal muscle, kidney and
 CC pancreas. Expressed in all epithelial and fibroblastic lines
 CC examined and in some, but not all, hematopoietic cells.
 CC -1- PTM: Phosphorylated by several receptor tyrosine kinases.
 CC -1- SIMILARITY: Contains 1 PH domain.
 CC -1- SIMILARITY: Contains 1 SH3 domain.
 CC -----
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 CC -----
 CC EMBL; U12535; AAA62280.1; -;
 DR PIR; I38728; I38728.
 DR HSSP; Q08509; IAOJ.
 DR Genew; HGNC:3420; EPS8.
 DR MIM; 60206; -;
 DR GO; GO:0005070; P:SH3/SH2 adaptor protein activity; TAS.
 DR GO; GO:0008283; P:cell proliferation; TAS.
 DR GO; GO:0007173; P:EGF receptor signaling pathway; TAS.
 DR GO; GO:0007165; P:signal transduction; TAS.
 DR InterPro; IPR006020; PTP_P1D.
 DR InterPro; IPR001452; SH3.
 DR Pfam; PF00018; SH3; 1.
 DR ProDom; PD000066; SH3; 1.
 DR SMART; SM00462; PTP; 1.
 DR SMART; SM00326; SH3; 1.
 DR PROSITE; PS50002; SH3; 1.
 DR SH3 domain; Phosphorylation.
 KW DOMAIN 69 129 PH (FIRST PART).
 FT DOMAIN 210 213 POLY-PRO.
 FT DOMAIN 321 325 POLY-PRO.
 FT DOMAIN 381 414 PH (SECOND PART).
 FT DOMAIN 421 440 PRO-RICH.
 FT DOMAIN 532 591 SH3.
 FT DOMAIN 615 651 PRO-RICH.
 FT DOMAIN 659 664 POLY-SER.
 SQ SEQUENCE 822 AA; 91881 MW; AC5EB1D28B784B3B CRC64;
 Query Match 72.7%; Score 32; DB 1; Length 822;
 Best Local Similarity 85.7%; Pred. No. 81;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 3 AELVHFL 9
 Db 355 ADLVHFL 361
 |:|||||
 |:|||||
 RESULT 29
 COAD STRPY STANDARD; PRT; 163 AA.
 ID PS8104;
 AC PS8104; (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Phosphatantethine adenyltransferase (EC 2.7.7.3) (Pantetheine-
 DE phosphate adenyltransferase) (PPAT) (Dephospho-CoA
 DE pyrophosphorylase).
 GN COAD OR KDTB OR SPI1537 OR SPYM3_1188 OR SPS0674 OR SPYM18_1554.
 OS Streptococcus pyogenes,
 OS Streptococcus pyogenes (serotype M3), and
 OS Streptococcus pyogenes (serotype M18).
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=1314, 198466, 186103;

RN SEQUENCE FROM N.A.
 RP STRAIN=SF370 / ATCC 700294 / Serotype M1;
 RC MEDLINE=21192684; PubMed=11296296;
 RX Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
 RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
 RA Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,
 RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
 RT "Complete genome sequence of an M1 strain of Streptococcus
 RT pyogenes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663 (2001).
 RN SEQUENCE FROM N.A.
 RP STRAIN=MGAS315 / Serotype M3;
 RC MEDLINE=22133808; PubMed=12122206;
 RX Beres S.B., Sylva G.L., Barbian K.D., Lei B., Hoff J.S.,
 RA Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D.,
 RA Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
 RA Schlievert P.M., Musser J.M.;
 RT "Genome sequence of a serotype M3 strain of group A Streptococcus:
 RT phage-encoded toxins, the high-virulence phenotype, and clone
 RT emergence.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083 (2002).
 RN SEQUENCE FROM N.A.
 RP STRAIN=SSI-1 / Serotype M3;
 RC MEDLINE=22683278; PubMed=12799345;
 RX Nakagawa I., Kurokawa K., Yamashita A., Nakata M., Tomiyasu Y.,
 RA Okahashi N., Kawabata S., Yamazaki K., Shiba T., Yasunaga T.,
 RA Hayashi H., Hattori M., Hamada S.;
 RT "Genome sequence of an M3 strain of Streptococcus pyogenes reveals a
 RT large-scale genomic rearrangement in invasive strains and new insights
 RT into phage evolution.";
 RL Genome Res. 13:1042-1055 (2003).
 RN SEQUENCE FROM N.A.
 RP STRAIN=MGAS8232 / Serotype M18;
 RC MEDLINE=21927593; PubMed=11917108;
 RX Smoot J.C., Barbian K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S.,
 RA Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F.,
 RA Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,
 RA Kapur V., Daly J.A., Veasey L.G., Musser J.M.;
 RT "Genome sequence and comparative microarray analysis of serotype M18
 RT group A Streptococcus strains associated with acute rheumatic fever
 RT outbreaks.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673 (2002).
 CC -1- FUNCTION: Reversibly transfers an adenylyl group from ATP to 4'-
 CC phosphopantetheine, yielding dephospho-CoA (dPCoA) and
 CC pyrophosphate (By similarity).
 CC -1- CATALYTIC ACTIVITY: ATP + pantetheine 4'-phosphate = diphosphate +
 CC 3'-dephospho-CoA.
 CC -1- PATHWAY: Coenzyme A (CoA) biosynthesis; fourth step.
 CC -1- SUBUNIT: Homohexamer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: Belongs to the bacterial coad family.
 CC -----
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 CC -----
 CC EMBL; A5006586; AAK34331.1; -;
 DR EMBL; A5014159; AAM79795.1; -;
 DR EMBL; A5005143; BAC63769.1; -;
 DR EMBL; A5010069; AAL98121.1; -;
 DR HSSP; P23875; 1B6T.
 DR HAMAP; MF 00151; -;
 DR InterPro; IPR004821; Cyt tran rel.
 DR InterPro; IPR004820; Cytidyltransf.
 DR InterPro; IPR001980; LPS_biosynth.


```
RP SEQUENCE FROM N.A.
RC STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Comerton P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holtroyd S., Jagels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Garra P., Parry C.,
RA Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrell B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18."
RL Nature 413:848-852(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Ty2 / ATCC 700931;
RX MEDLINE=22531367; PubMed=12644504;
RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
RA Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
RT and CT18."
RL J. Bacteriol. 185:2330-2337(2003).
CC -!- FUNCTION: The recF protein is involved in DNA metabolism; it is
CC required for DNA replication and normal SOS inducibility. RecF
CC binds preferentially to single-stranded, linear DNA. It also seems
CC to bind ATP (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the recF family.
CC -----
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CC -----
DR EMBL; AL627280; CAD03159.1; -
DR EMBL; AE016846; AAO71179.1; -
DR HAMAP; MF_00365; -; 1.
DR InterPro; IPR001238; RecF.
DR InterPro; IPR003395; SMC_N.
DR Pfam; PF02463; SMC_N; 1.
DR TIGRFAMs; TIGR00611; recf; 1.
DR PROSITE; PS00617; RECF_1; 1.
DR PROSITE; PS00618; RECF_2; 1.
DR DNA damage; DNA replication; DNA-binding; SOS response; DNA repair;
KW ATP-binding; Complete proteome.
FT INIT MET 0 0 BY SIMILARITY.
FT NP BIND 29 36 ATP (POTENTIAL).
SQ SEQUENCE 356 AA; 40338 MW; 06AFB80DFC49E319 CRC64;

Query Match 70.5%; Score 31; DB 1; Length 356;
Best Local Similarity 55.6%; Pred. No. 57;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KVAELVHFL 9
Db 103 KIAELAHLM 111

RESULT 34
REFC_SALTY STANDARD; PRT; 356 AA.
ID P24900;
AC 01-MAR-1992 (Rel. 21, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE DNA replication and repair protein recF.
GN RECF OR STM3836.
OS Salmonella typhimurium.
```

```
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92178981; PubMed=1542576;
RA Sandier S.J., Chackerian B., Li J.T., Clark A.J.;
RT "Sequence and complementation analysis of recF genes from Escherichia
RT coli, Salmonella typhimurium, Pseudomonas putida and Bacillus
RT subtilis: evidence for an essential phosphate binding loop."
RL Nucleic Acids Res. 20:839-845(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT LT2."
RL Nature 413:852-856(2001).
CC -!- FUNCTION: The recF protein is involved in DNA metabolism; it is
CC required for DNA replication and normal SOS inducibility. RecF
CC binds preferentially to single-stranded, linear DNA. It also seems
CC to bind ATP.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -!- SIMILARITY: Belongs to the recF family.
CC -----
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CC -----
DR EMBL; X62505; CA44366.1; -
DR EMBL; AE008878; AAL22695.1; -
DR PIR; S21057; S21057.
DR StyGene; SG10331; recF.
DR HAMAP; MF_00365; -; 1.
DR InterPro; IPR001238; RecF.
DR InterPro; IPR003395; SMC_N.
DR InterPro; IPR002017; Spectrin.
DR Pfam; PF02463; SMC_N; 1.
DR TIGRFAMs; TIGR00611; recf; 1.
DR PROSITE; PS00617; RECF_1; 1.
DR PROSITE; PS00618; RECF_2; 1.
DR DNA damage; DNA replication; DNA-binding; SOS response; DNA repair;
KW ATP-binding; Complete proteome.
FT INIT MET 0 0 BY SIMILARITY.
FT NP BIND 29 36 ATP (POTENTIAL).
FT CONFLICT 30 32 ANG -> DNA (IN REF. 1).
FT CONFLICT 106 107 EL -> DV (IN REF. 1).
FT CONFLICT 125 125 N -> T (IN REF. 1).
FT CONFLICT 165 165 R -> A (IN REF. 1).
FT CONFLICT 257 259 IRA -> MLC (IN REF. 1).
FT CONFLICT 286 286 E -> Q (IN REF. 1).
FT CONFLICT 295 295 MISSING (IN REF. 1).
FT CONFLICT 302 302 D -> A (IN REF. 1).
FT CONFLICT 310 310 A -> G (IN REF. 1).
FT CONFLICT 330 332 AIS -> EL (IN REF. 1).
SQ SEQUENCE 356 AA; 40382 MW; 5F7795ED97574EA5 CRC64;

Query Match 70.5%; Score 31; DB 1; Length 356;
Best Local Similarity 55.6%; Pred. No. 57;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KVAELVHFL 9
Db 103 KIAELAHLM 111
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```

Submitted (JUN-1993) to the EMBL/GenBank/DBJ databases.
[4]
RN INTERACTION WITH PDS1.
RX MEDLINE=21437412; PubMed=11553328;
RA Hilioi Z., Chung Y.-S., Mochizuki Y., Hardy C.F.J., Cohen-Fix O.;
RT "The anaphase inhibitor Pds1 binds to the APC/C-associated protein
RL Cdc20 in a destruction box-dependent manner.";
RN Curr. Biol. 11:1347-1352(2001).
[5]
RN REVIEW.
RX MEDLINE=22347229; PubMed=12459453;
RA Irniger S.;
RT "Cyclin destruction in mitosis: a crucial task of Cdc20.";
RN FEBS Lett. 532:7-11(2002).
CC -!- FUNCTION: Activator protein, which is required for proteolytic
CC destruction of cyclins during mitosis. Acts via its interaction
CC with the ubiquitin ligase APC/C complex. Plays an essential role
CC in mitosis exit by directing degradation of Clb2 cyclin. Also
CC required for two microtubule-dependent processes, nuclear
CC movements prior to anaphase and chromosome separation. CDC20 may
CC modulate microtubule structure either by promoting microtubule
CC disassembly or by altering the surface of the microtubules.
CC -!- SIMILARITY: Contains 7 WD repeats.
CC -!- CAUTION: Ref.1 sequence differs from that shown due to a
CC frameshift in position 502.
-----
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-----
DR EMBL; X59428; CAA42058.1; ALT_FRAME.
DR EMBL; Z72638; CAA96824.1; -.
DR EMBL; D16506; BAA03957.1; -.
DR PIR; S64126; S64126.
DR GerMOnline; 141164; -.
DR SGD; S0003084; CDC20.
DR InterPro; IPR000002; Fizzy.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 5.
DR ProDom; PD004563; Fizzy; 1.
DR SMART; SM00320; WD40; 5.
DR PROSITE; PS00678; WD_REPEATS_1; 4.
DR PROSITE; PS50082; WD_REPEATS_2; 2.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW Cell division; Mitosis; Activator; Microtubule; Repeat; WD repeat.
FT REPEAT 257 296
FT REPEAT 299 338
FT REPEAT 342 379
FT REPEAT 383 422
FT REPEAT 425 467
FT REPEAT 469 519
FT REPEAT 523 562
FT CONFLICT 318 319
FT CONFLICT 502 519
FT (IN REF. 1).
FT MISSING (IN REF. 1).
SQ SEQUENCE 610 AA; 67359 MW; CCE7CD149C1F5ACF CRC64;

Query Match 70.5%; Score 31; DB 1; Length 610;
Best Local Similarity 85.7%; Pred. No. 98;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVAELVH 7
Db 516 KVAELVH 522
|||||:|

RESULT 37
RRP3_THOGV

Submitted (JUN-1993) to the EMBL/GenBank/DBJ databases.
[4]
RN INTERACTION WITH PDS1.
RX MEDLINE=21437412; PubMed=11553328;
RA Hilioi Z., Chung Y.-S., Mochizuki Y., Hardy C.F.J., Cohen-Fix O.;
RT "The anaphase inhibitor Pds1 binds to the APC/C-associated protein
RL Cdc20 in a destruction box-dependent manner.";
RN Curr. Biol. 11:1347-1352(2001).
[5]
RN REVIEW.
RX MEDLINE=22347229; PubMed=12459453;
RA Irniger S.;
RT "Cyclin destruction in mitosis: a crucial task of Cdc20.";
RN FEBS Lett. 532:7-11(2002).
CC -!- FUNCTION: Activator protein, which is required for proteolytic
CC destruction of cyclins during mitosis. Acts via its interaction
CC with the ubiquitin ligase APC/C complex. Plays an essential role
CC in mitosis exit by directing degradation of Clb2 cyclin. Also
CC required for two microtubule-dependent processes, nuclear
CC movements prior to anaphase and chromosome separation. CDC20 may
CC modulate microtubule structure either by promoting microtubule
CC disassembly or by altering the surface of the microtubules.
CC -!- SIMILARITY: Contains 7 WD repeats.
CC -!- CAUTION: Ref.1 sequence differs from that shown due to a
CC frameshift in position 502.
-----
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-----
DR EMBL; X17873; CAA76908.1; -.
DR InterPro; IPR001591; Flu_PB2.
DR ProDom; PD001667; Flu_PB2; 1.
DR Transferase; RNA-directed RNA polymerase.
SQ SEQUENCE 769 AA; 88042 MW; 5301B3829ADE9595 CRC64;

Query Match 70.5%; Score 31; DB 1; Length 769;
Best Local Similarity 55.8%; Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KVAELVHFL 9
Db 236 RTAEVAHFL 244
|||||:|

RESULT 38
GYRA_HAEIN
ID GYRA_HAEIN STANDARD; PRT; 880 AA.
AC P43700;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE DNA gyrase subunit A (EC 5.99.1.3).
GN GYRA OR H1264.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Rd / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kervatage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Uterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Frichman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
```

RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.; genome random sequencing and assembly of Haemophilus influenzae
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
RL Rd.";
RL Science 269:496-512(1995).
CC -|- FUNCTION: DNA gyrase negatively supercoils closed circular double-
CC stranded DNA in an ATP-dependent manner and also catalyzes the
CC interconversion of other topological isomers of double-stranded
CC DNA rings, including catenanes and knotted rings.
CC -|- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining
CC of double-stranded DNA.
CC -|- SUBUNIT: Made up of two chains. The A chain is responsible for DNA
CC breakage and rejoining; the B chain catalyzes ATP hydrolysis. The
CC enzyme forms an A2B2 tetramer.
CC -----
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CC -----
CC EMBL; U32806; AAC22917.1; -;
CC PIR; E64113; E64113.
CC HSP; P09097; IAB4.
CC TIGR; H11264; -;
CC InterPro; IPR005743; DNA_GYRA.
CC InterPro; IPR006691; DNA_GYRASEA.C.
CC InterPro; IPR002205; DNA_topoisoIV.
CC Pfam; PF03989; DNA_GYRASEA.C; 6.
CC Pfam; PF00521; DNA_topoisoIV; 1.
CC ProDom; PD000742; DNA_topoisoIV; 1.
CC SMART; SM00434; TOP4c; 1.
CC TIGRFAMs; TIGR01063; gyrA; 1.
CC Topoisomerase; Isomerase; DNA-binding; Complete proteome.
KW ACT_SITE 123 123 123 DNA_CLEAVAGE [BY SIMILARITY].
FT ACT_SITE 123 123 123 MW; 0B2E9DD34155A322 CRC64;
SQ SEQUENCE 880 AA; 97818 MW; 0B2E9DD34155A322 CRC64;

Query Match 70.5%; Score 31; DB 1; Length 880;
Best Local Similarity 55.6%; Pred. No. 1.4e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVAELVHFL 9
|:|:|:|
Db 481 KIADLLHIL 489

RESULT 39
Y068 CAEEL STANDARD; PRT; 910 AA.
AC P34607;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein ZK1098.8 in chromosome III.
GN ZK1098.8.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodirinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favell A., Fraser A.,
RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
RA Johnston L., Jones A., Kershaw J., Kirsten J., Laister N.,
RA Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Showkeen R.,
RA Sims M., Smaison N., Smith A., Smith M., Sonnhammer E., Staden R.,
RA

RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
RA Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
RA Wohlman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RL elegans.";
RL Nature 368:32-38(1994).
CC -|- SIMILARITY: TO RIBONUCLEASE D.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
CC EMBL; Z22176; CAA80137.1; -;
CC PIR; S40930; S40930.
CC WormPep; ZK1098.8; CE00370.
CC InterPro; IPR002562; 3_5_exonuclease.
CC Pfam; PF01612; 3_5_exonuclease; 1.
CC SMART; SM00474; 35EXOC; 1.
KW Hypothetical protein.
SQ SEQUENCE 910 AA; 105569 MW; 5512D15423517FCD CRC64;

Query Match 70.5%; Score 31; DB 1; Length 910;
Best Local Similarity 55.6%; Pred. No. 1.5e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVAELVHFL 9
|:|:|:|
Db 551 KIADLLHIL 559

RESULT 40
SECA CHLTR
ID SECA_CHLTR STANDARD; PRT; 969 AA.
AC O84707;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Preprotein translocase secA subunit.
GN SECA OR CT701.
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D/UW-3/Cx;
RX MEDLINE=99008089; PubMed=9784136;
RA Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
RA Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
RA Davis R.W.;
RA "Genome sequence of an obligate intracellular pathogen of humans:
RT Chlamydia trachomatis.";
RL Science 282:754-759(1998).
CC -|- FUNCTION: Involved in protein export. Interacts with the secY/secE
CC subunits. SecA has a central role in coupling the hydrolysis of
CC ATP to the transfer of pre-secretory periplasmic and outer
CC membrane proteins across the membrane (By similarity).
CC -|- SUBUNIT: Part of the prokaryotic protein translocation apparatus
CC which comprise secA, secB, secD, secE, secF, secG and secY (By
CC similarity).
CC -|- SUBCELLULAR LOCATION: Cytoplasmic side of plasma membrane (By
CC similarity).
CC -----
CC -|- SIMILARITY: Belongs to the secA family.
CC -----
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CC -----
DR EMBL; AE001340; AAC68296.1; -.
DR PIR; G71482; G71482.
DR InterPro; IPR001650; Helicase_C.
DR InterPro; IPR00185; SecA.
DR Pfam; PF00271; Helicase_C; 1.
DR Pfam; PF01043; SecA_protein; 1.
DR PRINTS; PR00906; SECA.
DR TIGRFAMs; TIGR00963; secA; 1.
DR PROSITE; PS01312; SECA; 1.
KW Protein transport; ATP-binding; Membrane; Translocation; Transport;
KW Complete proteome.
FT NP_BIND 114 121 ATP (POTENTIAL).
SQ SEQUENCE 969 AA; 110358 MW; 2D551C2269EE86BE CRC64;

Query Match 70.5%; Score 31; DB 1; Length 969;
Best Local Similarity 75.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVAELVHF 8
Db 255 RVAELVYF 262

```

Search completed: July 23, 2004, 12:52:01
 Job time : 15 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 23, 2004, 12:48:16 ; Search time 35 Seconds
(without alignments)
81.133 Million cell updates/sec

Title: US-09-458-298b-711

Perfect score: 44

Sequence: 1 KVAELVHFL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25: *
1: sp_archaea: *
2: sp_bacteria: *
3: sp_fungi: *
4: sp_human: *
5: sp_invertebrate: *
6: sp_mammal: *
7: sp_mhc: *
8: sp_organelle: *
9: sp_phase: *
10: sp_plant: *
11: sp_rodent: *
12: sp_virus: *
13: sp_vertebrate: *
14: sp_unclassified: *
15: sp_rvirus: *
16: sp_bacteriap: *
17: sp_archaeap: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	100.0	315	4 Q7Z5K4	Q7Z5K4 homo sapien
2	44	100.0	315	4 Q8WHH6	Q8WHH6 homo sapien
3	39	88.6	163	16 Q67920	Q67920 aquifex ae
4	38	86.4	163	16 Q81XP4	Q81XP4 bacillus an
5	38	86.4	163	16 Q81GB3	Q81GB3 bacillus ce
6	38	86.4	169	16 Q9K7E0	Q9K7E0 bacillus ha
7	38	86.4	540	4 Q9NUL7	Q9NUL7 homo sapien
8	37	84.1	314	4 Q96E03	Q96E03 homo sapien
9	37	84.1	683	8 Q95G99	Q95G99 streptocac
10	37	84.1	2471	12 Q9YTR3	Q9YTR3 ateline her
11	36	81.8	163	16 Q8EJMO	Q8EJMO shewanella
12	36	81.8	177	4 Q9BZ80	Q9BZ80 homo sapien
13	36	81.8	184	16 Q9PCE5	Q9PCE5 xylella fas
14	36	81.8	184	16 Q87CN4	Q87CN4 xylella fas
15	36	81.8	252	16 Q93IA8	Q93IA8 rhizobium m
16	36	81.8	279	11 Q9D378	Q9D378 mus musculus

17	36	81.8	279	11 Q9CPR8	Q9CPR8 mus musculus
18	36	81.8	294	11 Q99PB1	Q99PB1 mus musculus
19	36	81.8	318	4 Q9BUN9	Q9BUN9 homo sapien
20	36	81.8	373	4 Q96D45	Q96D45 homo sapien
21	36	81.8	384	8 Q8HUM8	Q8HUM8 aphananthe
22	36	81.8	643	4 Q8TD91	Q8TD91 homo sapien
23	36	81.8	803	4 Q9UNY1	Q9UNY1 homo sapien
24	36	81.8	856	11 Q9R2C5	Q9R2C5 mus musculus
25	36	81.8	859	6 Q9NIE9	Q9NIE9 bos taurus
26	36	81.8	892	4 Q9YGF6	Q9YGF6 homo sapien
27	36	81.8	905	11 Q9WUX5	Q9WUX5 mus musculus
28	36	81.8	911	6 Q9NIF0	Q9NIF0 bos taurus
29	35	79.5	343	4 Q96M61	Q96M61 homo sapien
30	35	79.5	358	16 Q8ZR10	Q8ZR10 salmonella
31	35	79.5	400	11 Q91VT7	Q91VT7 mus musculus
32	35	79.5	715	4 Q9H6K9	Q9H6K9 homo sapien
33	35	79.5	729	11 Q99K30	Q99K30 mus musculus
34	35	79.5	743	4 Q9H6S3	Q9H6S3 homo sapien
35	34	77.3	140	5 Q817B8	Q817B8 echinococcu
36	34	77.3	210	16 Q8ZJ69	Q8ZJ69 yersinia pe
37	34	77.3	258	16 Q9ZV84	Q9ZV84 rhizobium m
38	34	77.3	317	4 Q14798	Q14798 homo sapien
39	34	77.3	660	8 Q9GDV6	Q9GDV6 veratrum vi
40	34	77.3	667	4 Q8NHV8	Q8NHV8 homo sapien
41	34	77.3	760	16 Q9FC45	Q9FC45 streptomyce
42	34	77.3	1174	13 Q7ZV56	Q7ZV56 xenopus lae
43	34	77.3	2477	12 Q80BL6	Q80BL6 salmeline
44	33	75.0	213	4 Q8TE16	Q8TE16 homo sapien
45	33	75.0	276	16 Q88Y59	Q88Y59 lactobacill

ALIGNMENTS

RESULT 1

Q7Z5K4 PRELIMINARY; PRT; 315 AA.

AC Q7Z5K4; PRELIMINARY; PRT; 315 AA.
DT 01-OCT-2003 (Tremblrel. 25, Created)
DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Melanoma antigen family A 9 (Fragment)
GN MAGEA9.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Zhu J., Feng Z., Guan X.;
RT "MAGE-9 antigen (MAGE9) gene expressed in human hepatocellular
RT carcinoma patients."
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY310325; AAF82171.1; -.
FT NON TER 315 315
SQ SEQUENCE 315 AA; 35116 MW; C9488470D409B96F CRC64;

Query Match 100.0%; Score 44; DB 4; Length 315;

Best Local Similarity 100.0%; Pred. No. 0.6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVAELVHFL 9

Db 111 KVAELVHFL 119

RESULT 2

Q8WHH6 PRELIMINARY; PRT; 316 AA.

AC Q8WHH6;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)

```

DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Tumor antigen MAGE-N.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Hepatoma;
RA Sui Y., Ye J., Wu W.;
RT "Cloning of a new gene of MAGE family in human hepatocellular
RT carcinoma.";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF443295; AAL37897.1; -.
DR InterPro; IPR002190; MAGE.
DR Pfam; PF01454; MAGE; 1.
DR PROSITE; PS00838; MAGE; 1.
SQ SEQUENCE 316 AA; 35409 MW; A463A9A740A089DF CRC64;

Query Match 100.0%; Score 44; DB 4; Length 316;
Best Local Similarity 100.0%; Pred. No. 0.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVAELVHFL 9
Db 112 KVAELVHFL 120

RESULT 3
O67920 PRELIMINARY; PRT; 163 AA.
ID O67920;
AC O67920;
DT 01-AUG-1998 (TReMBLrel. 07, Created)
DT 01-AUG-1998 (TReMBLrel. 07, Last sequence update)
DE 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Hypothetical protein AQ_2171.
GN AQ_2171.
OS Aquifex aeolicus.
OC Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
OX NCBI_TaxID=63363;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VF5;
RX MEDLINE=98196666; PubMed=9537320;
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.E., Overbeek R., Snead M.A., Keller M., Aufay M., Huber R.,
RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
RT aeolicus.";
RL Nature 392:353-358(1998).
DR EMBL; AE000776; AAC07894.1; -.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR006549; HAD-SF-IIIa.
DR InterPro; IPR008334; Hydrolase.
DR InterPro; IPR008230; Sugar Ptase.
DR Pfam; PF00702; Hydrolase; 1.
DR TIGRFAMs; TIGR01662; HAD-SF-IIIa; 1.
DR PIRSF; PIRSF006118; Sugar Ptase; 1.
DR PIRSF; PIRSF006118; Sugar Ptase; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 163 AA; 18356 MW; 7FD36C6D4E1F06BE CRC64;

Query Match 88.6%; Score 39; DB 16; Length 163;
Best Local Similarity 77.8%; Pred. No. 3.6;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVAELVHFL 9
Db 152 EVAEIHFLL 160

RESULT 4
Q81XP4 PRELIMINARY; PRT; 163 AA.
ID Q81XP4;
AC Q81XP4;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Hypothetical protein.
DE Hypothetical protein.
GN BA5189.
OS Bacillus anthracis (strain Ames).
OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus.
OX NCBI_TaxID=198094;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22608414; PubMed=12721629;
RA Read T.D., Peterson S.N., Tourasse N., Baillie L.W., Paulsen I.T.,
RA Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
RA Holtzapfel E.K., Okstad O.A., Helgason E., Ristone J., Wu M.,
RA Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.,
RA DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
RA Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.P.,
RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,
RA Hazen A., Cline R., Redmond C., Thwaite J.E., White O., Salzberg S.L.,
RA Thomson B., Friedlander A.M., Koehler T.M., Hanna P.C., Kolsto A.-B.,
RA Fraser C.M.;
RT "The genome sequence of Bacillus anthracis Ames and comparison to
RT closely related bacteria.";
RL Nature 423:81-86(2003).
DR EMBL; AE017040; AAP28858.1; -.
DR TIGR; BA5189; -.
DR InterPro; IPR002752; DUF64.
DR Pfam; PF01892; DUF64; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 163 AA; 18228 MW; 7B8F8515AD3C7CFF CRC64;

Query Match 86.4%; Score 38; DB 16; Length 163;
Best Local Similarity 87.5%; Pred. No. 5.9;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VAEVLVHFL 9
Db 25 IAEVLVHFL 32

RESULT 5
Q816B3 PRELIMINARY; PRT; 163 AA.
ID Q816B3;
AC Q816B3;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Low temperature requirement C protein.
GN BC4955.
OS Bacillus cereus (strain ATCC 14579 / DSM 31).
OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus.
OX NCBI_TaxID=226900;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22608415; PubMed=12721630;
RA Ivanova N., Sorokin A., Anderson I., Galleron N., Caudelon B.,
RA Kparal V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A.,
RA Chu L., Mazur M., Goltsman E., Larsen N., D'Souza M., Walunas T.,
RA Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,
RA Overbeek R., Kyrpides N.;
RT "Genome sequence of Bacillus cereus and comparative analysis with
RT Bacillus anthracis.";
RL Nature 423:87-91(2003).
DR EMBL; AE017014; AAP11827.1; -.
DR InterPro; IPR002752; DUF64.
DR Pfam; PF01892; DUF64; 1.
KW Complete proteome.
SQ SEQUENCE 163 AA; 18270 MW; ACOA38EE16057D4C CRC64;

Query Match 86.4%; Score 38; DB 16; Length 163;

```

```
Best Local Similarity 87.5%; Pred. No. 5.9;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VAEVLVHFL 9
Db 25 IAEVLVHFL 32

RESULT 6
Q9K7E0 PRELIMINARY; PRT; 169 AA.
AC Q9K7E0;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Low temperature requirement C protein.
GN BH3424.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125 / JCM 9153;
RX MEDLINE=20512582; PubMed=11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
halodurans and genomic sequence comparison with Bacillus subtilis.";
RL Nucleic Acids Res. 28:4317-4331(2000).
DR EMBL; AP001518; BAB07143.1; -.
DR PIR; H84077; H84077.
DR InterPro; IPR002752; DUF64.
DR Pfam; PF01892; DUF64; 1.
KW Complete proteome.
SQ SEQUENCE 169 AA; 18954 MW; 09C631B5162FA591 CRC64;

Query Match 86.4%; Score 38; DB 16; Length 169;
Best Local Similarity 87.5%; Pred. No. 6.1;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VAEVLVHFL 9
Db 25 IAEVLVHFL 32

RESULT 7
Q9NUL7 PRELIMINARY; PRT; 540 AA.
AC Q9NUL7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein FLJ11282 (Putative DEAD-box helicase MDDX28)
DE (DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 28).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA Nagatsuma M., Hozoi T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Negahari K., Masuho Y.,
RA Ninomiya K., Iwayanagi T.;
RT "NEDO human cDNA sequencing project.";
RN Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
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RA Valgardottir R., Brede G., Eide L.G., Frengen E., Prydz H.;
RT "Cloning and characterization of MDDX28, a putative DEAD-box helicase
with mitochondrial and nuclear localization.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
[3]
RN SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK002144; BAA92106.1; -.
DR EMBL; AF329821; AAG59833.1; -.
DR EMBL; BC024273; AAH24273.1; -.
DR Genew; HGNC:17330; DDX28.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0008026; F:ATP dependent helicase activity; IEA.
DR GO; GO:0016787; F:Nucleic acid binding; IEA.
DR GO; GO:0003676; F:Nucleic acid binding; IEA.
DR InterPro; IPR001410; DEAD.
DR InterPro; IPR001650; Helicase_C.
DR Pfam; PF00270; DEAD; 1.
DR Pfam; PF00271; helicase_C; 1.
DR SMART; SM00487; DEXDC; 1.
DR SMART; SM00490; HELIC; 1.
KW Hypothetical protein; ATP-binding; Helicase; Hydrolase.
SQ SEQUENCE 540 AA; 59551 MW; 19E8DA08203893B5 CRC64;

Query Match 86.4%; Score 38; DB 4; Length 540;
Best Local Similarity 88.9%; Pred. No. 19;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVAELVHFL 9
Db 377 KVAELVHFL 385

RESULT 8
Q96E03 PRELIMINARY; PRT; 314 AA.
AC Q96E03;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Similar to melanoma antigen, family A, 2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Adrenal gland;
RA Strausberg R.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013098; AAH13098.1; -.
DR InterPro; IPR002190; MAGE.
DR Pfam; PF01454; MAGE; 1.
DR PROSITE; PS00838; MAGE; 1.
SQ SEQUENCE 314 AA; 35024 MW; A94F16247D1BFBC0 CRC64;

Query Match 84.1%; Score 37; DB 4; Length 314;
Best Local Similarity 77.8%; Pred. No. 18;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVAELVHFL 9
Db 112 KVAELVHFL 120

RESULT 9
Q95G99 PRELIMINARY; PRT; 683 AA.
AC Q95G99;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
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01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DR NADH dehydrogenase F (Fragment).
 GN NDHF.
 OS Streptotachys ramosa.
 OG Chloroplast.
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 CC PACAD clade; Panicoideae; Paniceae; Streptotachys.
 OX NCBI_TaxID=158166;
 RN [1]
 SEQUENCE FROM N.A.
 RA Giussani L.M., Cota-Sanchez J.H., Zuloaga F.O., Kellogg E.A.;
 RP "A molecular phylogeny of the grass subfamily Panicoideae (Poaceae)
 RT shows multiple origins of C4 photosynthesis.";
 RL Am. J. Bot. 0:0-0(2001).
 DR EMBL; AY029686; AAK50525.1; -.
 DR GO; GO:0009507; C:chloroplast; IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0009523; C:photosystem II; IEA.
 DR GO; GO:0008137; F:NADH dehydrogenase (ubiquinone) activity; IEA.
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR GO; GO:0005215; F:transporter activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR GO; GO:0006120; P:mitochondrial electron transport, NADH to u. . .; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR003916; NADH_oxred5.
 DR InterPro; IPR001750; Oxidored_q1.
 DR InterPro; IPR002128; Oxidored_q1_C.
 DR InterPro; IPR001516; Oxidored_q1_N.
 DR InterPro; IPR005829; Sug transporter.
 DR Pfam; PF00361; oxidored_q1; 1.
 DR Pfam; PF01010; oxidored_q1_C; 1.
 DR Pfam; PF00662; oxidored_q1_N; 1.
 DR PRINTS; PR01434; NADH_OXNASE5.
 DR PROSITE; PS00217; SUGAR TRANSPORT 2; 1.
 KW NAD; Oxidoreductase; Plastoquinone; Chloroplast.
 FT NON_TER 683
 FT NON_TER 683
 SQ SEQUENCE 683 AA; 76675 MW; C49617F716205F5A CRC64;
 Query Match 84.1%; Score 37; DB 8; Length 683;
 Best Local Similarity 77.8%; Pred. No. 39;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 KVAELVHFL 9
 Db 663 KLAELTHFL 671
 RESULT 10
 ID Q9YTK3 PRELIMINARY; PRT; 2471 AA.
 AC Q9YTK3;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Large tegument protein.
 OS Ateine herpesvirus 3.
 CC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 CC Gammaherpesvirinae; Rhadinovirus.
 OX NCBI_TaxID=85616;
 RN [1]
 SEQUENCE FROM N.A.
 RA STRAIN=73;
 RC MEDLINE=20091363; PubMed=10623770;
 RA Albrecht J.C.;
 RT "Primary structure of the Herpesvirus Ateles genome.";
 RL J. Virol. 74:1033-1037(2000).
 RN [2]
 SEQUENCE FROM N.A.
 RA STRAIN=73;
 RC Albrecht J.-C., Fleckenstein B.;
 RA Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF083424; AAC95588.1; -.
 DR PIR; T42977; T42977.
 DR InterPro; IPR006928; Herpes teg N.
 DR Pfam; PF04843; Herpes teg N; 1.
 SQ SEQUENCE 2471 AA; 280025 MW; ACC1575FEE225B1D CRC64;
 Query Match 84.1%; Score 37; DB 12; Length 2471;
 Best Local Similarity 55.6%; Pred. No. 1.4e+02;
 Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KVAELVHFL 9
 Db 1520 KISELIHFI 1528
 RESULT 11
 ID Q8EJMO PRELIMINARY; PRT; 163 AA.
 AC Q8EJMO;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Transcriptional regulator, MerR family.
 GN S00443.
 OS Shewanella oneidensis.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
 OC Alteromonadaceae; Shewanella.
 OX NCBI_TaxID=70863;
 RN [1]
 SEQUENCE FROM N.A.
 RC STRAIN=MR-1;
 RX MEDLINE=22297686; PubMed=12368813;
 RA Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,
 RA Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A.,
 RA Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S.,
 RA Daou R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F.,
 RA Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M.,
 RA Matheravan J., Weidman J., Impraim M., Lee K., Berry K., Lee C.,
 RA Mueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A.,
 RA Feldblyum T.V., Smith H.O., Venter J.C., Neelson K.H., Fraser C.M.;
 RT "Genome sequence of the dissimilatory metal ion-reducing bacterium
 RT Shewanella oneidensis";
 RL Nat. Biotechnol. 20:1118-1123(2002).
 DR EMBL; AE015493; AAN53525.1; -.
 DR TIGR; S00443; -.
 DR GO; GO:0005622; C:intracellular; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR000551; HTH_MerR.
 DR Pfam; PF00376; merR; 1.
 DR PRINTS; PR00040; HTHMERR.
 DR SMART; SM00422; HTH_MERR; 1.
 DR PROSITE; PS00552; HTH_MERR_FAMILY; 1.
 KW Complete proteome.
 SQ SEQUENCE 163 AA; 17834 MW; 6DE0A3D55C2F2976 CRC64;
 Query Match 81.8%; Score 36; DB 16; Length 163;
 Best Local Similarity 75.0%; Pred. No. 16;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KVAELVHF 8
 Db 96 KIAELLHF 103
 RESULT 12
 ID Q9BZ80 PRELIMINARY; PRT; 177 AA.
 AC Q9BZ80;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE MAGE family testis and tumor-specific protein (Fragment).

GN MAGEC3
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RX MEDLINE=20321428; PubMed=10861452;
 RA Lucas S., De Plaen E., Boon T.;
 RT "MAGE-B5, MAGE-B6, MAGE-C2, and MAGE-C3: four new members of the MAGE
 family with tumor-specific expression.";
 RL Int. J. Cancer 87:55-60(2000).
 RN (2)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RA Lucas S., De Plaen E., Boon T.;
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF333706; AAK00358.1; -;
 DR InterPro; IPR002190; MAGE.
 DR Pfam; PF01454; MAGE; 1.
 DR PROSITE; PS00838; MAGE; 1.
 FT NON TER 1 177
 FT TER 177 177
 SQ SEQUENCE 177 AA; 19702 MW; FA141309E327C4A0 CRC64;

 Query Match 81.8%; Score 36; DB 4; Length 177;
 Best Local Similarity 88.9%; Pred. No. 17;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

 QY 1 KVAELVHFL 9
 DB 98 KVAELVQFL 106
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 RESULT 13
 Q9PCES PRELIMINARY; PRT; 184 AA.
 AC Q9PCES;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hypothetical protein Xf1836.
 GN Xf1836.
 OS Xylella fastidiosa.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
 OC Xanthomonadaceae; Xylella.
 OX NCBI_TaxID=2371;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=9a5c;
 RX MEDLINE=20365717; PubMed=10910347;
 RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
 RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
 RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
 RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,
 RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
 RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,
 RA Facinani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
 RA Fraga J.S., Franca S.C., Franco M.C., Frohne M., Furlan L.R.,
 RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
 RA Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
 RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
 RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
 RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
 RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
 RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
 RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.B.S.,
 RA Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
 RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
 RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
 RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
 RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,

RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
 RA da Silva J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
 RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuchioka M.H.,
 RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
 RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
 RT "The genome sequence of the plant pathogen Xylella fastidiosa";
 RL Nature 406:151-159(2000).
 DR EMBL; AE004005; AAF84642.1; -;
 DR PIR; A82631; A82631.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 184 AA; 19461 MW; 5D1D446EB2F73A03 CRC64;

 Query Match 81.8%; Score 36; DB 16; Length 184;
 Best Local Similarity 87.5%; Pred. No. 17;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

 QY 1 KVAELVHF 8
 DB 140 KVGELVHF 147
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 RESULT 14
 Q87CN4 PRELIMINARY; PRT; 184 AA.
 AC Q87CN4;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Conserved hypothetical protein.
 GN PD1031.
 OS Xylella fastidiosa (strain Temeculal / ATCC 700964).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
 OC Xanthomonadaceae; Xylella.
 OX NCBI_TaxID=183190;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22421331; PubMed=12533478;
 RA Van Sluys M.A., de Oliveira M.C., Monteiro-Vitorello C.B., Moon D.H.,
 RA Miyaki C.Y., Furlan L.R., Camargo L.E.A., da Silva A.C.R., da Silva F.R.,
 RA Takita M.A., Lemos E.G.M., Machado M.A., Ferro M.I.T., da Silva F.R.,
 RA Goldman M.H.S., Goldman G.H., Lemos M.V.F., El-Dorry H., Tsai S.M.,
 RA Carrer H., Carraro D.M., de Oliveira R.C., Nunes L.R., Siqueira W.J.,
 RA Coutinho L.L., Kimura E.T., Ferro E.S., Harakava R., Kuramae E.E.,
 RA Marino C.L., Gigliotti E., Abreu I.L., Alves L.M.C., do Amaral A.M.,
 RA Baia G.S., Blanco S.R., Brito M.S., Cannavan F.S., Celestino A.V.,
 RA da Cunha A.F., Fenille R.C., Ferro J.A., Formighieri E.P., Kishi L.T.,
 RA Leoni S.G., Oliveira A.R., Rosa V.E. Jr., Sasaki F.T., Sena J.A.D.,
 RA de Souza A.A., Truffi D., Tsukumo F., Yanai G.M., Zaros L.G.,
 RA Civerolo E.L., Simpson A.J.G., Almeida N.F. Jr., Setubal J.C.,
 RA Kitajima J.P.;
 RT "Comparative analyses of the complete genome sequences of Pierce's
 disease and citrus variegated chlorosis strains of Xylella
 fastidiosa";
 RL J. Bacteriol. 185:1018-1026(2003).
 DR EMBL; AE012557; AAO28891.1; -;
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 184 AA; 19509 MW; E642A9226D75F15A CRC64;

 Query Match 81.8%; Score 36; DB 16; Length 184;
 Best Local Similarity 87.5%; Pred. No. 17;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

 QY 1 KVAELVHF 8
 DB 140 KVGELVHF 147
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 RESULT 15
 Q931A8 PRELIMINARY; PRT; 252 AA.
 ID Q931A8
 AC Q931A8;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

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DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE SMA0074 protein.
GN RA0036 OR SMA0074.
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteri; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=21396509; PubMed=11481432;
RA Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,
RA Barloy-Hubler F., Bowser L., Capela D., Galibert F., Gouzy J.,
RA Gurjal M., Hong A., Huizar L., Hyman R.W., Kahn D., Kahn M.L.,
RA Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,
RA Yeh K.-C., Davis R.W., Federspiel N.A., Long S.R.;
RT "Nucleotide sequence and predicted functions of the entire
RT Sinorhizobium meliloti pSymA megaplasmid."
RL Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888 (2001).
DR EMBL; AE007198; AAK64694.1; -.
DR PIR; D95266; D95266.
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00080; SDEFAMILY.
DR PROSITE; PS00061; ADH_SHORT; 1. Complete proteome.
KW Plasmid; Hypothetical protein.
SQ SEQUENCE 252 AA; 26808 MW; 7D406C067435E9 CRC64;

Query Match 81.8%; Score 36; DB 16; Length 252;
Best Local Similarity 87.5%; Pred. No. 24;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VAEVLVHFL 9
Db 226 VADLVHFL 233

RESULT 16
ID Q9D378 PRELIMINARY; PRT; 279 AA.
AC Q9D378;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE 5730494G16RIK protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
RX MEDLINE=21095660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Stauber P., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohseki S.,
RA Hayashizaki Y.;
RP "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690 (2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo, and Embryonic stem cells;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Stauber P., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohseki S.,
RA Hayashizaki Y.;
RP "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690 (2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Mammary gland;
RX Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head, and Spinal cord;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium.

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RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohseki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690 (2001).
DR EMBL; AK018250; BAB31133.1; -.
DR MGD; MGI:1913897; 5730494G16RIK.
DR InterPro; IPR002190; MAGE.
DR Pfam; PF01454; MAGE; 1.
DR PROSITE; PS50838; MAGE; 1.
SQ SEQUENCE 279 AA; 31474 MW; 5E243590A99F15F0 CRC64;

Query Match 81.8%; Score 36; DB 11; Length 279;
Best Local Similarity 88.9%; Pred. No. 26;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVAELVHFL 9
Db 62 KVAELVQFL 70

RESULT 17
Q9CPR8 PRELIMINARY; PRT; 279 AA.
ID Q9CPR8
AC Q9CPR8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE 5730494G16RIK protein (MAGE-g1) (RIKEN CDNA 5730494G16 gene).
DR EMBL; AF007198; AAK64694.1; -.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo, and Embryonic stem cells;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Stauber P., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohseki S.,
RA Hayashizaki Y.;
RP "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690 (2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Mammary gland;
RX Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head, and Spinal cord;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium.

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RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RL 60,770 full-length cDNAs.";
RR Nature 420:563-573(2002).
DR EMBL; AK017727; BAB30899.1; -.
DR EMBL; AK010294; BAB26830.1; -.
DR EMBL; AF319979; AAK01207.1; -.
DR EMBL; BC034892; AAH34892.1; -.
DR EMBL; AK049759; BAC33907.1; -.
DR EMBL; AK076471; BAC36358.1; -.
DR MGD; MGI:1913897; 5730494G16R1k.
DR InterPro; IPR002190; MAGE.
DR Pfam; PF01454; MAGE; 1.
DR PROSITE; PS0838; MAGE; 1.
SQ SEQUENCE 279 AA; 31460 MW; F22435919BDG3160 CRC64;

Query Match 81.8%; Score 36; DB 11; Length 279;
Best Local Similarity 88.9%; Pred. No. 26;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVAELVHFL 9
Db 62 KVAELVQFL 70

RESULT 18
Q99PB1
ID AC Q99PB1 PRELIMINARY; PRT; 294 AA.
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE MAGE-G2.
GN 1700020D05RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Auchier P.H., Chomez P.M., De Backer O.R., Bertrand M.J.M.;
RT "Ten new murine members of the MAGE gene family.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF319980; AAK01208.1; -.
DR MGD; MGI:1922805; 1700020D05RIK.
DR InterPro; IPR002190; MAGE.
DR Pfam; PF01454; MAGE; 1.
DR PROSITE; PS0838; MAGE; 1.
SQ SEQUENCE 294 AA; 33442 MW; ED95F680DF3DE315 CRC64;

Query Match 81.8%; Score 36; DB 11; Length 294;
Best Local Similarity 88.9%; Pred. No. 28;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVAELVHFL 9
Db 78 KVAELVQFL 86

RESULT 19
Q9BUN9
ID AC Q9BUN9 PRELIMINARY; PRT; 318 AA.
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Skin antigen, family A, 8 (Melanoma antigen, family A, 8).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
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RC TISSUE=Skin;
RA Strauberg R.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RR [2]
RP SEQUENCE FROM N.A.
RA Kaline N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
RA Koundinya M., Raphael J., Moreira D., Kelley T., Labaer J., Lin Y.,
RA Phelan M., Farmer A.;
RT "Cloning of human full-length CDSs in BD Creator(TM) System Donor
RT vector.";
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002455; AAH02455.1; -.
DR EMBL; BC012744; AAH12744.1; -.
DR EMBL; BT007340; AAF36004.1; -.
DR InterPro; IPR002190; MAGE.
DR Pfam; PF01454; MAGE; 1.
DR PROSITE; PS0838; MAGE; 1.
SQ SEQUENCE 318 AA; 35214 MW; EA02C1FB42F6C080 CRC64;

Query Match 81.8%; Score 36; DB 4; Length 318;
Best Local Similarity 88.9%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVAELVHFL 9
Db 115 KVAELVHFL 123

RESULT 20
Q96D45
ID AC Q96D45 PRELIMINARY; PRT; 373 AA.
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Skin antigen, family E, 1, cancer/testis specific.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Strauberg R.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013318; AAH13318.1; -.
DR InterPro; IPR002190; MAGE.
DR Pfam; PF01454; MAGE; 1.
DR PROSITE; PS0838; MAGE; 1.
SQ SEQUENCE 373 AA; 41134 MW; 4AA51D8BA7EC499A CRC64;

Query Match 81.8%; Score 36; DB 4; Length 373;
Best Local Similarity 88.9%; Pred. No. 35;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVAELVHFL 9
Db 144 KVAELVHFL 152

RESULT 21
Q8HUM8
ID AC Q8HUM8 PRELIMINARY; PRT; 384 AA.
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE NADH dehydrogenase (Fragment).
GN NDHF.
OS Aphananthe aspera.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
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OC eurosids I; Rosales; Ulmaceae; Aphananthe.
OX NCBI_TaxID=63051;
RN [1]
RP SEQUENCE FROM N.A.
RA Sytsma K.J., Morawetz J., Pires J.C., Nepokroff M., Conti E.,
RA Zjhra M., Hall J.C., Chase M.W.;
RT "Urticalean rosids: circumscription, rosid ancestry, and phylogenetics
RT based on rbcL, trnL-F, and ndhF sequences.";
RL Am. J. Bot. 89:1531-1546(2002).
DR EMBL: AF500366; AAN63302.1; -. IEA.
DR GO: GO:0009507; C:chloroplast; IEA.
DR GO: GO:0008137; F:NADH dehydrogenase (ubiquinone) activity; IEA.
DR GO: GO:0006120; P:mitochondrial electron transport, NADH to u. . .; IEA.
DR InterPro: IPR003916; NADHb_oxred5.
DR InterPro: IPR01750; Oxidored_q1.
DR InterPro: IPR002128; Oxidored_q1_C.
DR Pfam: PF00361; oxidored_q1; 1.
DR Pfam: PF01010; oxidored_q1_C; 1.
DR PRINTS: PR01434; NADHbGNASE5.
KW Chloroplast.
FT NON TER 1 384
FT NON TER 384 384
SQ SEQUENCE 384 AA; 43581 MW; 8789DB112193AA60 CRC64;

Query Match 81.8%; Score 36; DB 8; Length 384;
Best Local Similarity 75.0%; Pred. No. 36;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVAELVHF 8
Db 365 KLAELIHF 372

RESULT 22
Q8TD91 08TD91 PRELIMINARY; PRT; 643 AA.
AC Q8TD91;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hepatocellular carcinoma-associated protein HCA2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Dong X.; Chen W.;
RT "Identification of genes in the chromosome X that are differentially
RT expressed in hepatocellular carcinoma.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF490508; AAM08355.1; -.
DR InterPro: IPR002190; MAGE.
DR Pfam: PF01454; MAGE; 2.
DR PROSITE: PS00838; MAGE; 2.
SQ SEQUENCE 643 AA; 71908 MW; 4BE342288B3FE8A6 CRC64;

Query Match 81.8%; Score 36; DB 4; Length 643;
Best Local Similarity 88.9%; Pred. No. 59;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVAELVHF 9
Db 459 KVAELVQFL 467

RESULT 23
Q9UNY1 09UNY1 PRELIMINARY; PRT; 803 AA.
AC Q9UNY1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE JAW1-related protein MRV1B short isoform.
GN MRV1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=99253648; PubMed=10321731;
RA Shaughnessy J.D. Jr., Largaespada D.A., Tian E., Fletcher C.F.,
RA Cho B.C., Vyas P., Jenkins N.A., Copeland N.G.;
RT "Mrv1, a common MRV integration site in BXH2 myeloid leukemias,
RT encodes a protein with homology to a lymphoid-restricted membrane
RT protein Jaw1.";
RL Oncogene 18:2069-2084(1999).
DR EMBL: AF081250; AAD25923.1; -.
DR InterPro: IPR008677; MRV1.
DR Pfam: PF05781; MRV1; 1.
DR PRINTS: PR01434; NADHbGNASE5.
SQ SEQUENCE 803 AA; 88078 MW; F1E19AC014EF3A30 CRC64;

Query Match 81.8%; Score 36; DB 4; Length 803;
Best Local Similarity 77.8%; Pred. No. 74;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVAELVHF 9
Db 724 KLEELVHFL 732

RESULT 24
Q9R2C5 09R2C5 PRELIMINARY; PRT; 856 AA.
AC Q9R2C5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE MRV1 protein.
GN MRV1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=99253648; PubMed=10321731;
RA Shaughnessy J.D. Jr., Largaespada D.A., Tian E., Fletcher C.F.,
RA Cho B.C., Vyas P., Jenkins N.A., Copeland N.G.;
RT "Mrv1, a common MRV integration site in BXH2 myeloid leukemias,
RT encodes a protein with homology to a lymphoid-restricted membrane
RT protein Jaw1.";
RL Oncogene 18:2069-2084(1999).
DR EMBL: U63407; AAD22568.1; -.
DR MGD; MGI:1338023; Mrv1.
DR InterPro: IPR008677; MRV1.
DR Pfam: PF05781; MRV1; 1.
DR PRINTS: PR01434; NADHbGNASE5.
SQ SEQUENCE 856 AA; 93264 MW; D6BCBFD701DB9A43 CRC64;

Query Match 81.8%; Score 36; DB 11; Length 856;
Best Local Similarity 77.8%; Pred. No. 78;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVAELVHF 9
Db 777 KLEELVHFL 785

RESULT 25
Q9N1E9 09N1E9 PRELIMINARY; PRT; 859 AA.
AC Q9N1E9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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DE IP3 receptor associated cGMP kinase substrate B.
GN IRAG.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20186769; PubMed=10724174;
RA Schlossmann J., Ammendola A., Ashman K., Zong X., Huber A.,
RA Neubauer G., Wang G.X., Allescher H.D., Korth M., Wilm M., Hofmann F.,
RA Ruth P.;
RT "Regulation of intracellular calcium by a signalling complex of IRAG,
RT IP3 receptor and cGMP kinase Ibeta.";
RL Nature 404:197-201(2000).
DR ENBL; AF195527; AAF61203.1; -.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR008677; MRV11.
DR Pfam; PF05781; MRV11; 1.
KW Kinase; Receptor.
SQ SEQUENCE 859 AA; 93136 MW; CDF33CF2EAFB99B2 CRC64;

Query Match 81.8%; Score 36; DB 6; Length 859;
Best Local Similarity 77.8%; Pred. No. 79;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVAELVHFL 9
Db 780 KLELVHFL 788
|: |||||
|: |||||

RESULT 26
Q9Y6F6 PRELIMINARY; PRT; 892 AA.
AC Q9Y6F6;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE JAW1-related protein MRV11A long isoform.
GN MRV11.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9253648; PubMed=10321731;
RA Shaughnessy J.D. Jr., Largaespada D.A., Tian E., Fletcher C.F.,
RA Cho B.C., Vyas P., Jenkins N.A., Copeland N.G.;
RT "Mrv11, a common MRV integration site in BXH2 myeloid leukemias,
RT encodes a protein with homology to a lymphoid-restricted membrane
RT protein Jaw1.";
RL Oncogene 18:2069-2084(1999).
DR ENBL; AF081249; AAD25922.1; -.
DR Genew; HGNC:7237; MRV11.
DR GO; GO:0005789; C:endoplasmic reticulum membrane; TAS.
DR InterPro; IPR008677; MRV11.
DR Pfam; PF05781; MRV11; 1.
SQ SEQUENCE 892 AA; 96981 MW; B67FAFBADCC1D9A6 CRC64;

Query Match 81.8%; Score 36; DB 4; Length 892;
Best Local Similarity 77.8%; Pred. No. 82;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVAELVHFL 9
Db 813 KLELVHFL 821
|: |||||
|: |||||

RESULT 27
Q9WUX5 PRELIMINARY; PRT; 905 AA.
AC Q9WUX5;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE MRV11A protein.
GN MRV11.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99253648; PubMed=10321731;
RA Shaughnessy J.D. Jr., Largaespada D.A., Tian E., Fletcher C.F.,
RA Cho B.C., Vyas P., Jenkins N.A., Copeland N.G.;
RT "Mrv11, a common MRV integration site in BXH2 myeloid leukemias,
RT encodes a protein with homology to a lymphoid-restricted membrane
RT protein Jaw1.";
RL Oncogene 18:2069-2084(1999).
DR ENBL; U63408; AAD22569.1; -.
DR MGD; MGI:1338023; Mrv11.
DR InterPro; IPR008677; MRV11.
DR Pfam; PF05781; MRV11; 1.
SQ SEQUENCE 905 AA; 98104 MW; E458EBF59224AE77 CRC64;

Query Match 81.8%; Score 36; DB 11; Length 905;
Best Local Similarity 77.8%; Pred. No. 83;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVAELVHFL 9
Db 826 KLELVHFL 834
|: |||||
|: |||||

RESULT 28
Q9N1F0 PRELIMINARY; PRT; 911 AA.
AC Q9N1F0;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE IP3 receptor associated cGMP kinase substrate A.
GN IRAGA.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20186769; PubMed=10724174;
RA Schlossmann J., Ammendola A., Ashman K., Zong X., Huber A.,
RA Neubauer G., Wang G.X., Allescher H.D., Korth M., Wilm M., Hofmann F.,
RA Ruth P.;
RT "Regulation of intracellular calcium by a signalling complex of IRAG,
RT IP3 receptor and cGMP kinase Ibeta.";
RL Nature 404:197-201(2000).
DR ENBL; AF195526; AAF61202.1; -.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR008677; MRV11.
DR Pfam; PF05781; MRV11; 1.
KW Kinase; Receptor.
SQ SEQUENCE 911 AA; 98375 MW; D743EFA5A28FF62D CRC64;

Query Match 81.8%; Score 36; DB 6; Length 911;
Best Local Similarity 77.8%; Pred. No. 83;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVAELVHFL 9
Db 832 KLELVHFL 840
|: |||||
|: |||||

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RESULT 29
Q96M61
ID Q96M61 PRELIMINARY; PRT; 343 AA.
AC Q96M61;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein FLJ32799.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Ishibashi T., Kanehori K., Yosida M., Watanabe S., Ishida S., Ono Y.,
RA Hotuta T., Hiraoka S., Murakawa K., Takiguchi S., Kusano J.,
RA Watanabe M., Fujimori K., Tanai H., Ishida M., Yamashita H., Chiba Y.,
RA Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S.,
RA Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,
RA Kimura K., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
RA Wgatsuma M., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,
RA Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Strauberg R.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK057361; BAB71450.1; -.
DR EMBL; BC029525; AAH29525.1; -.
DR InterPro; IPR002190; MAGE.
DR Pfam; PF01454; MAGE; 1.
DR PROSITE; PS0838; MAGE; 1.
KW Hypothetical protein.
SQ SEQUENCE 343 AA; 38522 MW; C1E9286D8545EC87 CRC64;

Query Match 79.5%; Score 35; DB 4; Length 343;
Best Local Similarity 77.8%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KVAELVHFL 9
|||
DB 110 KVSIVHFL 118
|||||

RESULT 30
Q8ZR10
ID Q8ZR10 PRELIMINARY; PRT; 358 AA.
AC Q8ZR10;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Citrate lyase synthetase (Citrate (pro-3S)-lyase ligase
DE (EC 6.2.1.22)).
GN CITC OR STM0624.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Flores L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
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LT2.";
RL Nature 413:852-856 (2001).
DR EMBL; AE008724; AAL19575.1; -.
DR GO; GO:0016874; F:ligase activity; IEA.
DR GO; GO:0016829; F:lyase activity; IEA.
DR GO; GO:0008080; F:N-acetyltransferase activity; IEA.
DR GO; GO:0008771; F:ictrate (pro-3S)-lyase ligase activity; IEA.
DR InterPro; IPR005216; Cit_ly_ligase.
DR InterPro; IPR004821; Cyt_tran_rel.
DR InterPro; IPR000182; GCN5acetyl_trans.
DR Pfam; PF00583; Acetyltransf; 1.
DR TIGRFAMS; TIGR00124; cit_ly_ligase; 1.
DR TIGRFAMS; TIGR00125; cyt_tran_rel; 1.
KW Lyase; Ligase; Complete proteome.
SQ SEQUENCE 358 AA; 40443 MW; 823CCFD7C90CDD56 CRC64;

Query Match 79.5%; Score 35; DB 16; Length 358;
Best Local Similarity 66.7%; Pred. No. 54;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVAELVHFL 9
|||
DB 17 KMAEIAHFL 25
|||||

RESULT 31
Q91VT7
ID Q91VT7 PRELIMINARY; PRT; 400 AA.
AC Q91VT7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN EPS8L2 OR AI042819.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Breast tumor;
RA Strauberg R.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC009098; AAH09098.1; -.
DR MGD; MGI:2138828; Eps8L2.
DR InterPro; IPR006020; PTB_PID.
DR PROSITE; PS01179; PID; 1.
KW Hypothetical protein.
SQ SEQUENCE 400 AA; 44839 MW; E50B9205E139ECEF CRC64;

Query Match 79.5%; Score 35; DB 11; Length 400;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AELVHFL 9
|||||
DB 344 AELVHFL 350
|||||

RESULT 32
Q9H6K9
ID Q9H6K9 PRELIMINARY; PRT; 715 AA.
AC Q9H6K9;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein FLJ22171 (Epidermal growth factor receptor
DE pathway substrate 8 related protein 2).
GN EPS8R2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
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DR SMART; SMO0054; EFH; 4.
DR PROSITE; PS00018; EF HAND; 4.
SQ SEQUENCE 140 AA; 15595 MW; 908648B6652B361E CRC64;

Query Match 77.3%; Score 34; DB 5; Length 140;
Best Local Similarity 77.8%; Pred. No. 35;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVAELVHFL 9
Db 91 EVAEKHFLL 99

RESULT 36
Q8ZJ69 PRELIMINARY; PRT; 210 AA.
AC Q8ZJ69;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Putative two-component response regulator (Response
DE regulator/transcription activator).
GN YPO0235 OR Y0512.
OS Yersinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CO-92 / Biovar Orientalis;
RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
RA Prentice M.B., Sebahia M., James K.D., Churcher C., Mungall K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Fellwell T., Hamlin N., Holroyd S., Jagsis K., Karlyshev A.V.,
RA Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
RT "Genome sequence of Yersinia pestis, the causative agent of plague.";
RL Nature 413:523-527(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=KIM5 / Biovar Mediaevalis;
RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
RA Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V., Blattner F.R.,
RA Straley S.C., McDonough K.A., Nilles M.D., Matson J.S., Perry R.D.;
RT "Genome sequence of Yersinia pestis KIM.";
RL J. Bacteriol. 184:4601-4611(2002).
DR EMBL; AJ414141; CAC89116.1; -.
DR EMBL; AE013653; AAM84101.1; -.
DR PIR; A10031; A10031.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0000156; P:two-component response regulator activity; IEA.
DR GO; GO:0000160; P:two-component signal transduction system (p. . .); IEA.
DR InterPro; IPR000792; HTH_LuxR.
DR InterPro; IPR001789; Response_reg.
DR Pfam; PF00196; GerE; 1.
DR Pfam; PF00072; response_reg; 1.
DR PRINTS; PR00038; HTHLUXR.
DR ProDom; PD000307; HTH_LuxR; 1.
DR ProDom; PD000039; Response_reg; 1.
DR PROSITE; PS00622; HTH_LUXR_FAMILY; 1.
DR PROSITE; PS00110; RESPONSE_REGULATORY; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 210 AA; 23575 MW; 051170240F203DBE CRC64;

Query Match 77.3%; Score 34; DB 16; Length 210;
Best Local Similarity 75.0%; Pred. No. 53;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 KVAELVHF 8
Db 195 KVAELIHW 202

RESULT 37
Q92V84 PRELIMINARY; PRT; 258 AA.
AC Q92V84;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Putative oxidoreductase, SDR superfamily protein.
GN RH0825 OR SMD21159.
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=21396508; PubMed=11481431;
RA Finan T.M., Weidner S., Wong K., Buhrmester J., Chain P.,
RA Vorhoeelter F.J., Hernandez-Lucas I., Becker A., Cowie A., Goury J.,
RA Golding B., Puehler A.;
RT "The complete sequence of the 1.683-kb pSymb megaplasmid from the N2-
RT fixing endosymbiont Sinorhizobium meliloti";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894(2001).
DR EMBL; AL603645; CAC49225.1; -.
DR PIR; A95945; A95945.
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR002196; ADH_short.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00080; SDRFAMILY.
DR PROSITE; PS00061; ADH_SHORT; 1.
KW Plasmid; Hypothetical protein; Complete proteome.
SQ SEQUENCE 258 AA; 27066 MW; 2A9824BE86044A4E CRC64;

Query Match 77.3%; Score 34; DB 16; Length 258;
Best Local Similarity 87.5%; Pred. No. 64;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 VAELVHFL 9
Db 215 VAELVHFL 222

RESULT 38
Q14798 PRELIMINARY; PRT; 317 AA.
AC Q14798;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE MAGE-4 protein.
GN MELANOMA ANTIGEN-4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95369706; PubMed=7642112;
RA Imai Y., Shichijo S., Yamada A., Katayama T., Yano H., Itoh K.;
RT "Sequence analysis of the MAGE gene family encoding human tumor-
RT rejection antigens.";
RL Gene 160:287-290(1995).
DR EMBL; D32075; BAA06841.1; -.
DR InterPro; IPR002190; MAGE.

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